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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/51, C07K 14/18, G01N 33/53, A61K 39/29, C12Q 1/68, 1/70, C07K 16/10		A3	(11) International Publication Number: WO 96/05315
			(43) International Publication Date: 22 February 1996 (22.02.96)
(21) International Application Number: PCT/US95/10398			(81) Designated States: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TT, UA, UG, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG), ARIPO patent (KE, MW, SD, SZ, UG).
(22) International Filing Date: 15 August 1995 (15.08.95)			
(30) Priority Data: 08/290,665 15 August 1994 (15.08.94) US			
(71) Applicant: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, represented by THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES, Office of Technology Transfer National Institutes of Health [US/US]; Suite 325, 6011 Executive Boulevard, Rockville, MD 20852 (US).			
(72) Inventors: BUKH, Jens; 5805 Sonoma Road, Bethesda, MD 20817 (US). MILLER, Roger, H.; 15504 White Willow Lane, Rockville, MD 20853 (US). PURCELL, Robert, H.; 17517 White Grounds Road, Boyds, MD 20841 (US).			Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
(74) Agent: FEILER, William, S.; Morgan & Finnegan, L.L.P., 345 Park Avenue, New York, NY 10154 (US).			
(88) Date of publication of the international search report: 4 April 1996 (04.04.1996)			

(54) Title: NUCLEOTIDE AND AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF HEPATITIS C VIRUS

(57) Abstract

The nucleotide and deduced amino acid sequences of cDNAs encoding the envelope (1) genes and core genes of isolates of hepatitis C virus (HCV) are disclosed. The invention relates to the oligonucleotides, peptides and recombinant envelope (1) and core proteins derived from these sequences and their use in diagnostic methods and vaccines.

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FR	France			VN	Viet Nam
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INTERNATIONAL SEARCH REPORT

International Application No

PC 1/US 95/10398

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/51 C07K14/18 G01N33/53 A61K39/29 C12Q1/68
 C12Q1/70 C07K16/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K G01N A61K C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	PROC. NATL. ACAD. SCI. USA., vol. 89, no. 11, June 1992 pages 4942-4946, JENS BUKH ET AL. 'Sequence analysis of the 5' noncoding region of hepatitis C virus.'	1,2,21, 31,32,38
Y	see the whole document	5-20, 22-30, 33-37, 39-51, 53,54, 56-59

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☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

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P document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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Date of the actual completion of the international search

20 February 1996

Date of mailing of the international search report

01.03.96

Name and mailing address of the ISA

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Hix, R

INTERNATIONAL SEARCH REPORT

Inter. natl. Application No.
PCT/US 95/10398

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	PROC NATL ACAD SCI U S A 90 (17). 1993. 8234-8238. CODEN: PNASA6 ISSN: 0027-8424, September 1993 BUKH J ET AL 'AT LEAST 12 GENOTYPES OF HEPATITIS C VIRUS PREDICTED BY SEQUENCE ANALYSIS OF THE PUTATIVE E1 GENE OF ISOLATES COLLECTED WORLDWIDE.'	1,2,5, 21-23, 26-32,38
Y	see the whole document	5-20,24, 25, 33-37, 39-51, 53,54, 56-59
X	--- JOURNAL OF GENERAL VIROLOGY 75 (5). 1994. 1053-1061. ISSN: 0022-1317, May 1994 SIMMONDS P ET AL 'Identification of genotypes of hepatitis C virus by sequence comparisons in the core, E1 and NS-5 regions.'	21,28
Y	see the whole document	1,2, 5-20, 22-27, 29-51, 53,54, 56-59
X	--- JOURNAL OF BIOMEDICAL SCIENCE 1 (3). 1994. 158-162. ISSN: 1021-7770, June 1994 KAO J-H ET AL 'Detection of divergent hepatitis C virus envelope sequences.'	21,28
Y	see the whole document	1,2, 5-20, 22-27, 29-51, 53,54, 56-59
X	--- BIOCHEM BIOPHYS RES COMMUN 192 (2). 1993. 635-641. CODEN: BBRC A9 ISSN: 0006-291X, 30 April 1993 STUYVER L ET AL 'ANALYSIS OF THE PUTATIVE E1 ENVELOPE AND NS4A EPITOPE REGIONS OF HCV TYPE 3.'	21,28
Y	see the whole document	1,2, 5-20, 22-27, 29-51, 53,54, 56-59

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 95/10398

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ARCHIVES OF VIROLOGY SUPPLEMENTUM 0 (7). 1993. 27-39. ISSN: 0939-1983. ROGGENDORF M ET AL 'Variability of the envelope regions of HCV in European isolates and its significance for diagnostic tools.'	21,28
Y	see the whole document	1,2, 5-20, 22-27, 29-51, 53,54, 56-59
X	--- PROC. NATL. ACAD. SCI. U. S. A. (1992), 89(15), 7144-8 CODEN: PNASA6;ISSN: 0027-8424, 1 August 1992 CHA, T. A. ET AL 'At least five related, but distinct, hepatitis C viral genotypes exist'	21,28
Y	see the whole document	1,2, 5-20, 22-27, 29-51, 53,54, 56-59
X	--- BIOCHEM. BIOPHYS. RES. COMMUN. (1994), 199(3), 1474-81 CODEN: BBRCA9;ISSN: 0006-291X, 30 March 1994 LI, JI-SU ET AL 'Identification of the third major genotype of hepatitis C virus in France'	21,28
Y	see the whole document	1,2, 5-20, 22-27, 29-51, 53,54, 56-59
X	--- WO,A,94 01778 (CHIRON CORP) 20 January 1994	53,54, 56-58
Y	see the whole document	1,2, 5-51,59
X	--- WO,A,92 19743 (CHIRON CORP) 12 November 1992	21,28
Y	see the whole document	1,2, 5-20, 22-27, 29-51, 53,54, 56-59
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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 95/10398

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO,A,92 21759 (PASTEUR INSTITUT) 10 December 1992 see the whole document ---	1,2, 5-51,53, 54,56-59
X	EP,A,0 586 065 (TONEN CORP) 9 March 1994 see the whole document ---	53,54, 56-58
X	PROC. NATL. ACAD. SCI. USA, vol. 89, January 1992 pages 187-191, J. BUKH ET AL 'Importance of primer selection for the detection of hepatitis C virus RNA with the polymerase chain reaction assay' see the whole document ---	21,28
P,X	WO,A,95 01442 (US HEALTH) 12 January 1995 see the whole document ---	1,2, 5-51,53, 54,56-59
P,X	WO,A,94 25601 (INNOGENETICS NV ;MAERTENS GEERT (BE); STUYVER LIEVEN (BE)) 10 November 1994 see the whole document ---	21,28
Y	see the whole document ---	1,2, 5-20, 22-27, 29-51, 53,54, 56-59
P,X	WO,A,94 27153 (CHIRON CORP) 24 November 1994 see the whole document ---	21,28, 53-58
Y	see the whole document ---	1,2, 5-20, 22-27, 29-51,59
P,X	PROC. NATL. ACAD. SCI. U. S. A. (1994), 91(21), 10134-8 CODEN: PNASA6;ISSN: 0027-8424, 11 October 1994 STUYVER, LIEVEN ET AL 'Classification of hepatitis C viruses based on phylogenetic analysis of the envelope 1 and nonstructural 5B regions and identification of five additional subtypes' see the whole document ---	1,2, 5-51,53, 54,56-59

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 95/10398

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	JOURNAL OF CLINICAL MICROBIOLOGY 32 (9). 1994. 2280-2284. ISSN: 0095-1137, September 1994 RAVAGGI A ET AL 'Distribution of viral genotypes in Italy determined by hepatitis C virus typing by DNA immunoassay.' see the whole document ---	1,2, 5-51,53, 54,56-59
P,X	SEMINARS IN LIVER DISEASE, vol. 15, no. 1, February 1995 pages 41-63, J. BUKH ET AL. 'Genetic Heterogeneity of hepatitis C virus: Quasispecies and genotypes' see the whole document ---	1,2, 5-51,53, 54,56-59
P,X	BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 202, no. 3, 15 August 1994 pages 1308-1314, L. STUYVER 'Cloning and phylogenetic analysis of the core, E2 and NS3/NS4 regions of the hepatitis C virus type 5a+' see the whole document -----	1,2, 5-51,53, 54,56-59

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 95/10398

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 18, 45, 49
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although these claims are directed to a method of treatment of (diagnostic method practised on) the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

- 26 subjects

See continuation-sheets PCT/ISA/210

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1, 2, 5-51, 53, 54, 56-59 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

claims:

1. 1,2,5-51,53,54,56 to 59 (partially):

Genotypes specific peptides from E1 Seq. ID 1-8 and 52-59 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype I/1a.

2. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 103-108 and 155-160 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype I/1a.

3. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 9-25 and 60-76 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype II/1b.

4. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 109-124 and 161-176 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype II/1b.

5. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 26-29 and 77-80 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype III/2a.

6. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 125-128 and 177-180 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype III/2a.

7. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 30-33 and 81-84 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype IV/2b.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

8. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 129-133 and 181-185 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype IV/2b.

9. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 34 and 85 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype IV/2c.

10. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 134 and 186 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype IV/2c.

11. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 35-39 and 86-90 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype V/3a.

12. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 135-138 and 187-190 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype V/3a.

13. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 40 and 91 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4a.

14. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 139 and 191 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4a.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

15. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 41 and 92 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4b.

16. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 141 and 193 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4b.

17. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 42-43 and 93-94 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4c.

18. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 143-144 and 195-196 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4c.

19. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 44 and 95 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4d.

20. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 145 and 197 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4d.

21. 3-52,55 and 59 (partially):

Genotype specific peptides Core Seq. ID 142 and 194 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4e.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

22. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 140 and 192 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4f.

23. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 45-50 and 96-101 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 5a.

24. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. 146-153 and 198-205 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 5a.

25. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 51 and 102 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 6a.

26. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 154 and 206 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 6a.

INTERNATIONAL SEARCH REPORT

information on patent family members

International Application No

PCT/US 95/10398

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A-9401778	20-01-94	AU-B- 4662993 EP-A- 0649537 FI-A- 950002 HU-A- 70473 JP-T- 7509060 NO-A- 950006 PL-A- 307178 SK-A- 495	31-01-94 26-04-95 27-02-95 30-10-95 05-10-95 24-02-95 02-05-95 11-07-95
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WO-A-9427153	24-11-94	NONE	



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/51, C07K 14/18, G01N 33/53, A61K 39/29, C12Q 1/68, 1/70, C07K 16/10	A3	(11) International Publication Number: WO 96/05315 (43) International Publication Date: 22 February 1996 (22.02.96)
(21) International Application Number: PCT/US95/10398 (22) International Filing Date: 15 August 1995 (15.08.95) (30) Priority Data: 08/290,665 15 August 1994 (15.08.94) US (71) Applicant: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, represented by THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES, Office of Technology Transfer National Institutes of Health [US/US]; Suite 325, 6011 Executive Boulevard, Rockville, MD 20852 (US). (72) Inventors: BUKH, Jens; 5805 Sonoma Road, Bethesda, MD 20817 (US). MILLER, Roger, H.; 15504 White Willow Lane, Rockville, MD 20853 (US). PURCELL, Robert, H.; 17517 White Grounds Road, Boyds, MD 20841 (US). (74) Agent: FEILER, William, S.; Morgan & Finnegan, L.L.P., 345 Park Avenue, New York, NY 10154 (US).		(81) Designated States: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TT, UA, UG, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG), ARIPO patent (KE, MW, SD, SZ, UG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 4 April 1996 (04.04.1996)
(54) Title: NUCLEOTIDE AND AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF HEPATITIS C VIRUS		
(57) Abstract <p>The nucleotide and deduced amino acid sequences of cDNAs encoding the envelope (1) genes and core genes of isolates of hepatitis C virus (HCV) are disclosed. The invention relates to the oligonucleotides, peptides and recombinant envelope (1) and core proteins derived from these sequences and their use in diagnostic methods and vaccines.</p>		

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- 1 -

Title of the InventionNUCLEOTIDE AND AMINO ACID SEQUENCES
OF THE ENVELOPE 1 AND CORE GENES
OF HEPATITIS C VIRUS

The present application is a continuation-in-part of pending U.S. Application Serial No. 08/086/428, filed on June 29, 1993.

Field Of Invention

The present invention is in the field of hepatitis virology. The invention relates to the complete nucleotide and deduced amino acid sequences of the envelope 1 (E1) and core genes of hepatitis C virus (HCV) isolates from around the world and the grouping of these isolates into fourteen distinct HCV genotypes. More specifically, this invention relates to oligonucleotides, peptides and recombinant proteins derived from the envelope 1 and core gene sequences of these isolates of hepatitis C virus and to diagnostic methods and vaccines which employ these reagents.

Background Of Invention

Hepatitis C, originally called non-A, non-B hepatitis, was first described in 1975 as a disease serologically distinct from hepatitis A and hepatitis B (Feinstone, S.M. et al. (1975) N. Engl. J. Med. 292:767-770). Although hepatitis C was (and is) the leading type of transfusion-associated hepatitis as well as an important part of community-acquired hepatitis, little progress was made in understanding the disease until the recent identification of hepatitis C virus (HCV) as the causative agent of hepatitis C via the cloning and sequencing of the HCV genome (Choo, A.L. et al. (1989) Science 288:359-362). The sequence information generated by this study resulted

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° in the characterization of HCV as a small, enveloped, positive-stranded RNA virus and led to the demonstration that HCV is a major cause of both acute and chronic hepatitis worldwide (Weiner, A.J. et al. (1990) Lancet 335:1-3). These observations, combined with studies
5 showing that over 50% of acute cases of hepatitis C progress to chronicity with 20% of these resulting in cirrhosis and an undetermined proportion progressing to liver cancer, have led to tremendous efforts by investigators within the hepatitis C field to develop
10 diagnostic assays and vaccines which can detect and prevent hepatitis C infection.

The cloning and sequencing of the HCV genome by Choo et al. (1989) has permitted the development of serologic tests which can detect HCV or antibody to HCV
15 (Kuo, G. et al. (1989) Science 244:362-364). In addition, the work of Choo et al. has also allowed the development of methods for detecting HCV infection via amplification of HCV RNA sequences by reverse transcription and cDNA polymerase chain reaction (RT-PCR) using primers derived
20 from the HCV genomic sequence (Weiner, A.J. et al.). However, although the development of these diagnostic methods has resulted in improved diagnosis of HCV infection, only approximately 60% of cases of hepatitis C are associated with a factor identified as contributing to
25 transmission of HCV (Alter, M.J. et al. (1989) JAMA 262:1201-1205). This observation suggests that effective control of hepatitis C transmission is likely to occur only via universal pediatric vaccination as has been initiated recently for hepatitis B virus. Unfortunately, attempts to
30 date to protect chimpanzees from hepatitis C infection via administration of recombinant vaccines have had only limited success. Moreover, the apparent genetic heterogeneity of HCV, as indicated by the recent assignment of all available HCV isolates to one of four genotypes, I-
35 IV (Okamoto, H. et al. (1992) J. Gen. Virol; 73:673-679),

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- ° presents additional hurdles which must be overcome in order to develop accurate and effective diagnostic assays and vaccines.

For example, one possible obstacle to the development of effective hepatitis C vaccines would arise if the observed genetic heterogeneity of HCV reflects serologic heterogeneity. In such a case, the most genetically diverse strains of HCV may then represent different serotypes of HCV with the result being that infection with one strain may not protect against infection with another. Indeed, the inability of one strain to protect against infection with another strain was recently noted by both Farci et al. (Farci, P. et al. (1992) Science 258:135-140) and Prince et al. (Prince, A.M. et al. (1992) J. Infect. Dis. 165:438-443), each of whom presented evidence that while infection with one strain of HCV does modify the degree of the hepatitis C associated with the reinfection, it does not protect against reinfection with a closely related strain. The genetic heterogeneity among different HCV strains also increases the difficulty encountered in developing RT-PCR assays to detect HCV infection since such heterogeneity often results in false-negative results because of primer and template mismatch. In addition, currently used serologic tests for detection of HCV or for detection of antibody to HCV are not sufficiently well developed to detect all of the HCV genotypes which might exist in a given blood sample. Finally, in terms of choosing the proper treatment modality to combat hepatitis infection, the inability of presently available serologic assays to distinguish among the various genotypes of HCV represents a significant shortcoming in that recent reports suggest that an HCV-infected patient's response to therapy might be related to the genotype of the infectious virus (Yoshioka, K. et al. (1992) Hepatology 16:293-299; Kanai, K. et al. (1992) Lancet 339:1543; Lan, J.Y.N. et al. (1992) Hepatology 16:209A). Indeed, the data

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° presented in the above studies suggest that the closely related genotypes I and II are less responsive to interferon therapy than are the closely related genotypes III and IV. Moreover, preliminary data by Pozzato et al. (Pozzato, G. et al. (1991) Lancet 338:509) suggests that
5 different genotypes may be associated with different types or degrees of clinical disease. Taken together, these studies suggest that before effective vaccines against HCV infection can be developed, and indeed, before more accurate and effective methods for diagnosis and treatment
10 of HCV infection can be produced, one must obtain a greater knowledge about the genetic and serologic diversity of HCV isolates.

In a recent attempt to gain an understanding of the extent of genetic heterogeneity among HCV strains, Bukh et al. carried out a detailed analysis of HCV isolates via
15 the use of PCR technology to amplify different regions of the HCV genome (Bukh, J. et al. (1992a) Proc. Natl. Acad. Sci. 89:187-191). Following PCR amplification, the 5'-noncoding (5' NC) portion of the genomes of various HCV
20 isolates were sequenced and it was found that primer pairs designed from conserved regions of the 5' NC region of the HCV genome were more sensitive for detecting the presence of HCV than were primer pairs representing other portions of the genome (Bukh, J. et al. (1992b) Proc. Natl. Acad.
25 Sci. U.S.A. 89:4942-4946). In addition, the authors noted that although many of the HCV isolates examined could be classified into the four genotypes described by Okamoto et al. (1992), other previously undescribed genotypes emerged based on genetic heterogeneity observed in the 5' NC region
30 of the various isolates. One of the most prominent of these newly noted genotypes comprised a group of related viruses that contained the most genetically divergent 5' NC regions of those studied. This group of viruses, tentatively classified as a fifth genotype, are very
35 similar to strains recently described by others (Cha, T.-A

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° et al. (1992) Proc. Natl. Acad. Sci. U.S.A. 89:7144-7148;
Chan, S-W. et al. (1992) J. Gen. Virol., 73:1131-1141 and
Lee, C-H et al. (1992) J. Clin. Microbio. 30:1602-1604).
In addition, at least four more putative genotypes were
identified thereby providing evidence that the genetic
5 heterogeneity of HCV was more extensive than previously
appreciated.

However, while the studies of Bukh et al. (1992a
and b) provided new and useful information on the genetic
heterogeneity of HCV, it is widely appreciated by those
10 skilled in the art that the three structural genes of HCV,
core (C), envelope (E1) and envelope 2/nonstructural 1
(E2/NS1) are the most important for the development of
serologic diagnostics and vaccines since it is the product
of these genes that constitutes the hepatitis C virion.
15 Thus, a determination of the nucleotide sequence of one or
all of the structural genes of a variety of HCV isolates
would be useful in designing reagents for use in diagnostic
assays and vaccines since a demonstration of genetic
heterogeneity in a structural gene(s) of HCV isolates might
20 suggest that some of the HCV genotypes represent distinct
serotypes of HCV based upon the previously observed
relationship between genetic heterogeneity and serologic
heterogeneity among another group of single-stranded,
positive-sense RNA viruses, the picornaviruses (Ruechert,
25 R.R. "Picornaviridae and their replication", in Fields,
B.N. et al., eds. Virology, New York: Raven Press, Ltd.
(1990) 507-548).

Summary of Invention

30 The present invention relates to cDNAs encoding
the complete nucleotide sequence of either the envelope 1
(E1) gene or the core (C) gene of an isolate of human
hepatitis C virus (HCV).

The present invention also relates to the nucleic
35 acid and deduced amino acid sequences of these E1 and core

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° cDNAs.

It is an object of this invention to provide synthetic nucleic acid sequences capable of directing production of recombinant E1 and core proteins, as well as equivalent natural nucleic acid sequences. Such natural
5 nucleic acid sequences may be isolated from a cDNA or genomic library from which the gene capable of directing synthesis of the E1 or core proteins may be identified and isolated. For purposes of this application, nucleic acid sequence refers to RNA, DNA, cDNA or any synthetic variant
10 thereof which encodes for peptides.

The invention also relates to the method of preparing recombinant E1 and core proteins derived from E1 and core cDNA sequences respectively by cloning the nucleic acid encoding either the recombinant E1 or core protein and
15 inserting the cDNA into an expression vector and expressing the recombinant protein in a host cell.

The invention also relates to isolated and substantially purified recombinant E1 and core proteins and analogs thereof encoded by E1 and core cDNAs respectively.

20 The invention further relates to the use of recombinant E1 and core proteins, either alone, or in combination with each other, as diagnostic agents and as vaccines.

The present invention also relates to the
25 recombinant production of the core protein of the present invention to contain a second protein on its surface and therefore serve as a carrier in a multivalent vaccine preparation. Further, the present invention relates to the use of the self aggregating core or envelope proteins as a
30 drug delivery system for anti-virals.

The invention also relates to the use of single-stranded antisense poly- or oligonucleotides derived from E1 or core cDNAs, or from both E1 and core cDNAs, to inhibit expression of hepatitis C E1 and/or core genes.

35 The invention further relates to multiple

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° computer-generated alignments of the nucleotide and deduced amino acid sequences of the E1 and core cDNAs. These multiple sequence alignments produce consensus sequences which serve to highlight regions of homology and non-homology between sequences found within the same genotype or in different genotypes and hence, these alignments can be used by one skilled in the art to design peptides and oligonucleotides useful as reagents in diagnostic assays and vaccines.

10 The invention therefore also relates to purified and isolated peptides and analogs thereof derived from E1 and core cDNA sequences.

The invention further relates to the use of these peptides as diagnostic agents and vaccines.

15 The present invention also encompasses methods of detecting antibodies specific for hepatitis C virus in biological samples. The methods of detecting HCV or antibodies to HCV disclosed in the present invention are useful for diagnosis of infection and disease caused by HCV and for monitoring the progression of such disease. Such methods are also useful for monitoring the efficacy of therapeutic agents during the course of treatment of HCV infection and disease in a mammal.

20 The invention also provides a kit for the detection of antibodies specific for HCV in a biological sample where said kit contains at least one purified and isolated peptide derived from the E1 or core cDNA sequences. In addition, the invention provides for a kit containing at least one purified and isolated peptide derived from the E1 cDNA sequences and at least one purified and isolated peptide derived from the core cDNA sequences.

25 The invention further provides isolated and purified genotype-specific oligonucleotides and analogs thereof derived from E1 and core cDNA sequences.

35 The invention also relates to methods for

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detecting the presence of hepatitis C virus in a mammal, said methods comprising analyzing the RNA of a mammal for the presence of hepatitis C virus. The invention further relates to methods for determining the genotype of hepatitis C virus present in a mammal. This method is useful in determining the proper course of treatment for an HCV-infected patient.

The invention also provides a diagnostic kit for the detection of hepatitis C virus in a biological sample. The kit comprises purified and isolated nucleic acid sequences useful as primers for reverse-transcription polymerase chain reaction (RT-PCR) analysis of RNA for the presence of hepatitis C virus genomic RNA.

The invention further provides a diagnostic kit for the determination of the genotype of a hepatitis C virus present in a mammal. The kit comprises purified and isolated nucleic acid sequences useful as primers for RT-PCR analysis of RNA for the presence of HCV in a biological sample and purified and isolated nucleic acid sequences useful as hybridization probes in determining the genotype of the HCV isolate detected in PCR analysis.

This invention also relates to pharmaceutical compositions useful in prevention or treatment of hepatitis C in a mammal.

Description of Figures

Figures 1A-1 thru 1H-5 show computer generated sequence alignments of the nucleotide sequences of 51 HCV E1 cDNAs. The single letter abbreviations used for the nucleotides shown in Figures 1A-1 thru 1H-5 are those standardly used in the art. Figures 1A-1 thru 1A-10 show the alignment of SEQ ID NOs:1-8 to produce a consensus sequence for genotype I/1a. Figures 1B-1 thru 1B-10 show the alignment of SEQ ID NOs:9-25 to produce a consensus sequence for genotype II/1b. Figures 1C-1 thru 1C-5 show the alignment of SEQ ID NOs:26-29 to produce a consensus

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sequence for genotype III/2a. Figures 1D-1 thru 1D-5 show the alignment of SEQ ID NOs:30-33 to produce a consensus sequence for genotype IV/2b. Figures 1E-1 thru 1E-5 show the alignment of SEQ ID NOs:35-39 to produce a consensus sequence for genotype V/3a. Figures 1F-1 thru 1F-3 show the computer alignment of SEQ ID NOs:42-43 to produce a "consensus" sequence for genotype 4C where the "consensus" sequence given is that of SEQ ID NO:42. Figures 1G-1 thru 1G-5 show the alignment of SEQ ID NOs:45-50 to produce a consensus sequence for genotype 5a. The nucleotides shown in capital letters in the consensus sequences of Figures 1A-1 thru 1G-5' are those conserved within a genotype while nucleotides shown in lower case letters in the consensus sequences are those variable within a genotype. In addition, in Figures 1A-1 thru 1E-5 and 1G-1 thru 1G-5, when the lower case letter is shown in a consensus sequence, the lower case letter represents the nucleotide found most frequently in the sequences aligned to produce the consensus sequence. In Figures 1F-1 thru 1F-3, the lower case letters shown in the consensus sequence are nucleotides in SEQ ID NO:42 which differ from nucleotides found in the same positions in SEQ ID NO:43. Finally, a hyphen at a nucleotide position in the consensus sequences in Figures 1A-1 thru 1G-5 indicates that two nucleotides were found in equal numbers at that position in the aligned sequences. In the aligned sequences, nucleotides are shown in lower case letters if they differed from the nucleotides of both adjacent isolates. Figures 1H-1 thru 1H-5 show the alignment of the consensus sequences of Figures 1A-1 thru 1G-5 with SEQ ID NO:34 (genotype 2c), SEQ ID NO:40 (genotype 4a), SEQ ID NO:41 (genotype 4b), SEQ ID NO:44 (genotype 4d) and SEQ ID NO:51 (genotype 6a) to produce a consensus sequence for all twelve genotypes. This consensus sequence is shown as the bottom line of Figures 1H-1 thru 1H-5 where the nucleotides shown in capital letters are conserved among all genotypes and a

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blank space indicates that the nucleotide at that position is not conserved among all genotypes.

Figures 2A-1 thru 2H-2 show computer alignments of the deduced amino acid sequences of 51 HCV E1 cDNAs. The single letter abbreviations used for the amino acids shown in Figures 2A-1 thru 2H-2 follow the conventional amino acid shorthand for the twenty naturally occurring amino acids. Figures 2A-1 thru 2A-4 show the alignment of SEQ ID NOs:52-59 to produce a consensus sequence for genotype I/1a. Figures 2B-1 thru 2B-4 show the alignment of SEQ ID NOs:60-76 to produce a consensus sequence for genotype II/1b. Figures 2C-1 and 2C-2 show the alignment of SEQ ID NOs:77-80 to produce a consensus sequence for genotype III/2a. Figures 2D-1 and 2D-2 show the alignment of SEQ ID NOs:81-84 to produce a consensus sequence for genotype IV/2b. Figures 2E-1 and 2E-2 show the alignment of SEQ ID NOs:86-90 to produce a consensus sequence for genotype V/3a. Figure 2F-1 shows the computer alignment of SEQ ID NOs:93-94 to produce a consensus sequence for genotype 4c. Figures 2G-1 and 2G-2 show the alignment of SEQ ID NOs:96-101 to produce a consensus sequence for genotype 5a. The amino acids shown in capital letters in the consensus sequences of Figures 2A-1 thru 2G-2 are those conserved within a genotype while amino acids shown in lower case letters in the consensus sequences are those variable within a genotype. In addition, in Figures 2A-1 thru 2E-2 and 2G-1 thru 2G-2 when the lower case letter is shown in a consensus sequence, the letter represents the amino acid found most frequently in the sequences aligned to produce the consensus sequence. In Figure 2F-1, the lower case letters shown in the consensus sequence are amino acids in SEQ ID NO:93 which differ from amino acids found in the same positions in SEQ ID NO:94. Finally, a hyphen at an amino acid position in the consensus sequences of Figures 2A-1 thru 2G-2 indicates that two amino acids were found in equal numbers at that position

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in the aligned sequences. In the aligned sequences, amino acids are shown in lower case letters if they differed from the amino acids of both adjacent isolates. Figures 2H-1 and 2H-2 show the alignment of the consensus sequences of Figures 2A-1 thru 2G-2 with SEQ ID NO:85 (genotype 2c), SEQ ID NO:91 (genotype 4a), SEQ ID NO:92 (genotype 4b), SEQ ID NO:95 (genotype 4d) and SEQ ID NO:102 (genotype 6a) to produce a consensus sequence for all twelve genotypes. This consensus sequence is shown as the bottom line of Figures 2H-1 and 2H-2 where the amino acids shown in capital letters are conserved among all genotypes and a blank space indicates that the amino acid at that position is not conserved among all genotypes.

Figures 3A and 3B show multiple sequence alignment of the deduced amino acid sequence of the E1 gene of 51 HCV isolates collected worldwide. The consensus sequence of the E1 protein is shown in boldface (top). In the consensus sequence cysteine residues are highlighted with stars, potential N-linked glycosylation sites are underlined, and invariant amino acids are capitalized, whereas variable amino acids are shown in lower case letters. In the alignment, amino acids are shown in lower case letters if they differed from the amino acid of both adjacent isolates. Amino acid residues shown in bold print in the alignment represent residues which at that position in the amino acid sequence are genotype-specific. Amino acids that were invariant among all HCV isolates are shown as hyphens (-) in the alignment. Amino acid positions correspond to those of the HCV prototype sequence (HCV-1, Choo, L. et al. (1991) Proc. Natl. Acad. Sci. USA 88:2451-2455) with the first amino acid of the E1 protein at position 192. The grouping of isolates into 12 genotypes (I/1a, II/1b, III/2a, IV/2b, V/3a, 2c, 4a, 4b, 4c, 4d, 5a and 6a) is indicated.

Figure 4 shows a dendrogram of the genetic

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relatedness of the twelve genotypes of HCV based on the percent amino acid identity of the E1 gene of the HCV genome. The twelve genotypes shown are designated as I/1a, II/1b, III/2a, IV/2b, V/3a, 2c, 4a, 4b, 4c, 4d, 5a and 6a. The shaded bars represent a range showing the maximum and minimum homology between the amino acid sequence of any one isolate of the genotype indicated and the amino acid sequence of any other isolate.

Figure 5 shows the distribution of the complete E1 gene sequence of 74 HCV isolates into the twelve HCV genotypes in the 12 countries studied. For 51 of these HCV isolates, including 8 isolates of genotype I/1a, 17 isolates of genotype II/1b and 26 isolates comprising the additional 10 genotypes, the complete E1 gene sequence was determined. In the remaining 23 isolates, all of genotypes I/1a and II/1b, the genotype assignment was based on only a partial E1 gene sequence. The partially sequenced isolates did not represent additional genotypes in any of the 12 countries. The number of isolates of a particular genotype is given in each of the 12 countries studied. For ease of viewing, those genotypes designated by two terms (e.g., I/1a) are indicated by the latter term (e.g. 1a). The designations used for each country are: Denmark (DK); Dominican Republic (DR); Germany (D); Hong Kong (HK); India (IND); Sardinia, Italy (S); Peru (P); South Africa (SA); Sweden (SW); Taiwan (T); United States (US); and Zaire (Z). National borders depicted in this figure represent those existing at the time of sampling.

Figures 6A-1 thru 6K-2 show computer generated sequence alignments of the nucleotide sequences of 52 HCV core cDNAs. Single letter abbreviations used for the nucleotides shown in Figures 6A-1 thru 6J-4 are those standardly used in the art. Figures 6A-1 thru 6A-4 show the alignment of SEQ ID NOs: 103-108 to produce a consensus sequence for genotype I/1a. Figures 6B-1 thru 6B-10 show the alignment of SEQ ID NOs: 109-124 to produce

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a consensus sequence for genotype II/1b. Figures 6C-1 thru 6C-10 show the alignments of the sequences comprising minor genotypes I/1a (SEQ ID NOS: 103-108) and II/1b (SEQ ID NOS: 109-124) to produce a consensus sequence for the major genotype, genotype 1. Figures 6D-1 thru 6D-3 show the alignment of SEQ ID NOS: 125-128 to produce a consensus sequence for genotype III/2a. Figures 6E-1 thru 6E-4 show the alignment of SEQ ID NOS: 129-133 to produce a consensus sequence for genotype IV/2b. Figures 6F-1 thru 6F-5 show the alignment of the sequences of minor genotypes III/2a (SEQ ID NOS: 125-128), IV/2b (SEQ ID NOS: 129-133) and 2c (SEQ ID NO: 134) to produce a consensus sequence for the major genotype, genotype 2. Figures 6G-1 thru 6G-3 show the alignment of SEQ ID NOS: 135-138 to produce a consensus sequence for genotype V/3a. Figures 6H-1 thru 6H-4 show the computer alignment of the sequences of minor genotypes 4a-4f (SEQ ID NOS: 139-145) to produce a consensus sequence for the major genotype, genotype 4. Figures 6I-1 thru 6I-4 show the alignment of SEQ ID NOS: 146-153 to produce a consensus sequence for genotype 5a. The nucleotides shown in capital letters in the consensus sequences in Figures 6A-1 thru 6I-4 are those conserved within the genotype while nucleotides shown in lower case letters in the consensus sequences are those variable within a genotype. In addition, when the lower case letter is shown in the consensus sequence, the lower case letter represents the nucleotide found most frequently in the sequences aligned to produce that consensus sequence. Moreover, a hyphen at a nucleotide position in the consensus sequences in Figures 6A-1 thru 6I-4 indicates that two nucleotides were found in equal numbers at that position in the sequences aligned to produce the consensus sequence. Finally, nucleotides are shown in lower case letters in the sequences aligned to produce each consensus sequence shown in Figures 6A-1 thru 6I-4, if they differed from the nucleotides of both

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adjacent isolates. Figures 6J-1 thru 6-14 show the alignment of the consensus sequences of major genotypes 1 (Figures 6C-1 thru 6C-10), 2 (Figures 6F-1 thru 6F-5), 3 (Figures 6G-1 thru 6G-3), 4 (Figures 6H-1 thru 6H-4), 5 (Figures 6I-1 thru 6I-4) and 6 (SEQ ID NO: 154) to produce a consensus sequence for all genotypes and Figures 6K-1 and 6K-2 show the alignment of consensus sequences of Figures 6A-1 thru 6A-4, 6B-1 thru 6B-10, 6D-1 thru 6D-3, 6E-1 thru 6E-4, 6G-1 thru 6G-3 and 6I-1 thru 6I-4 with SEQ ID NO:134 (genotype 2c), SEQ ID NO:139 (genotype 4a), SEQ ID NO:141 (genotype 4b), SEQ ID NO:143 (genotype 4c), SEQ ID NO:145 (genotype 4d), SEQ ID NO:142 (genotype 4e), SEQ ID NO:140 (genotype 4f) and SEQ ID NO:154 (genotype 6a) to produce a consensus sequence for all fourteen genotypes. The nucleotides shown in capital letters in the consensus sequences of Figures 6J-1 thru 6K-2 are conserved among all genotypes and the nucleotide shown in lower case letter represent the nucleotides found most frequently in the sequences aligned to produce this consensus sequence. In addition, the presence of a hyphen at a nucleotide position in all fourteen sequences aligned in Figures 6K-1 and 6K-2 indicates that the nucleotide found at that position in the aligned sequences is the same as nucleotide shown at the corresponding position in the consensus sequences of Figure 6K.

Figures 7A-1 thru 7J-1 show computer alignments of the deduced amino acid sequences of the 52 HCV core cDNAs. The single letter abbreviations used for the amino acids shown in Figures 7A-1 thru 7J-1 follow the conventional amino acid short hand for the twenty natural occurring amino acids. Figures 7A-1 and 7A-2 show the alignment of SEQ ID NOs: 155-160 to produce a consensus sequence for genotype I/1a. Figures 7B-1 and 7B-2 show the alignment of SEQ ID NOs: 161-176 to produce a consensus sequence for genotype II/1b. Figures 7C-1 thru 7C-4 show the alignment of the sequences comprising minor

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° genotypes I/a (SEQ ID NOS: 155-160) and II/1b (SEQ ID NOS: 161-176) to produce a consensus sequence for the major genotype, genotype 1. Figure 7D-1 shows the alignment of SEQ ID NOS: 177-180 to produce a consensus sequence for genotype III/2a. Figure 7E-1 shows the alignment of SEQ ID NOS: 181-185 to produce a consensus sequence for genotype IV/2b. Figures 7F-1 and 7F-2 show the alignment of the sequences of minor genotypes III/2a (SEQ ID NOS: 177-180), IV/2b (SEQ ID NOS: 181-185) and 2c (SEQ ID NO: 186) to produce a consensus sequence for the major genotype, genotype 2. Figure 7G-1 shows the alignment of SEQ ID NOS: 187-190 to produce a consensus sequence for genotype V/3a. Figures 7H-1 and 7H-2 shows the computer alignment of the sequences of minor genotypes 4a-4f (SEQ ID NOS: 191-197) to produce a consensus sequence for the major genotype, genotype 4. Figures 7I-1 and 7I-2 show the alignment of SEQ ID NOS: 198-205 to produce a consensus sequence for genotype 5a. The amino acids shown in capital letters in the consensus sequences of Figures 7A-1 thru 7I-2 are those conserved within the genotype while amino acids shown in lower case letters in the consensus sequences are those variable within the genotype. In addition, when a lower case letter is found in the consensus sequences shown in Figures 7A-1 thru 7I-2, the letter represents the amino acid found most frequently in the sequences aligned to produce that consensus sequence. Moreover, a hyphen in an amino acid position in the consensus sequences of Figures 7A-1 thru 7I-2 indicates that two amino acids were found in equal numbers at that position in the sequences aligned to produce that consensus sequence. Finally, amino acids are shown in lower case letters in the sequences aligned to produce the consensus sequences shown in Figures 7A-1 thru 7I-2 if these amino acids differed from the amino acids of both adjacent isolates. Figure 7J-1 shows the alignment of the consensus sequences of major genotypes 1 (Figures

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7C-1 thru 7C-4), 2 (Figure 7F-1), 3 (Figure 7G-1), 4 (Figures 7H-1 and 7H-2), 5 (Figures 7I-1 and 7I-2) and 6 (SEQ ID NO: 154) to produce a consensus sequence for all genotypes and Figure 7K-1 shows the alignment of the consensus sequences of Figures 7A-1 and 7A-2, 7B-1 and 7B-2, 7D-1, 7E-1, 7G-1 and 7I-1 and 7I-2 with SEQ ID NO:186 (genotype 2c), SEQ ID NO:191 (genotype 4a), SEQ ID NO:193 (genotype 4b), SEQ ID NO:195 (genotype 4c), SEQ ID NO:197 (genotype 4d), SEQ ID NO:194 (genotype 4e), SEQ ID NO:192 (genotype 4f) and SEQ ID NO:206 (genotype 6a) to produce a consensus sequence for all fourteen genotypes. The amino acids shown in capital letters in the consensus sequences shown in Figures 7J-1 and 7K-1 are conserved among all genotypes while the amino acids shown in lower case letters represent amino acids found most frequently in the sequences aligned to produce this consensus sequence. In addition, the presence of a hyphen at an amino acid position in all fourteen sequences aligned in Figure 7K-1 indicates that the amino acid found at that position in the aligned sequences is the same as the amino acid shown at the corresponding position in the consensus sequence of Figure 7K-1.

Figures 8A and 8B show phylogenetic trees illustrating the calculated evolutionary relationships of the different HCV isolates based upon the C gene sequence of 52 HCV isolates (Figure 8A) and the E1 gene sequence of 51 HCV isolates (Figure 8B), respectively. The phylogenetic trees were constructed by the unweighted pair-group method with arithmetic mean (Nei, M. (1987) *Molecular Evolutionary Genetics* (Columbia University Press, New York, N.Y.), pp 287-326) using the computer software package "Gene Works" from IntelliGenetics. The lengths of the horizontal lines connecting the sequences, given in absolute values from 0 to 1, are proportional to the estimated genetic distances between the sequences. Genotype designations of HCV isolates are indicated. In 45

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- ° HCV isolates, both the C and the E1 gene sequences were determined.

Detailed Description Of Invention

5 The present invention relates to cDNAs encoding the complete nucleotide sequence of the envelope 1 (E1) and core genes of isolates of human hepatitis C virus (HCV). The E1 cDNAs of the present invention were obtained as follows. Viral RNA was extracted from serum collected from humans infected with hepatitis C virus and 10 the viral RNA was then reverse transcribed and amplified by polymerase chain reaction using primers deduced from the sequence of the HCV strain H-77 (Ogata, N. et al. (1991) Proc. Natl. Acad. Sci. U.S.A. 88:3392-3396). The amplified cDNA was then isolated by gel electrophoresis and sequenced. 15

The present invention further relates to the nucleotide sequences of the cDNAs encoding the E1 gene of 51 HCV isolates. These nucleotide sequences are shown in the sequence listing as SEQ ID NO:1 through SEQ ID NO:51.

20 The abbreviations used for the nucleotides are those standardly used in the art.

The deduced amino acid sequence of each of SEQ ID NO:1 through SEQ ID NO:51 are presented in the sequence listing as SEQ ID NO:52 through SEQ ID NO:102 where the 25 amino acid sequence in SEQ ID NO:52 is deduced from the nucleotide sequence shown in SEQ ID NO:1, the amino acid sequence shown in SEQ ID NO:53 is deduced from the nucleotide sequence shown in SEQ ID NO:2 and so on. The deduced amino acid sequence of each of SEQ ID Nos:52-102 starts at nucleotide 1 of the corresponding nucleic acid 30 sequence shown in SEQ ID NOs:1-51 and extends 575 nucleotides to a total length of 576 nucleotides.

The three letter abbreviations used in SEQ ID Nos:52-102 follow the conventional amino acid shorthand 35 for the twenty naturally occurring amino acids..

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The present invention also relates to the nucleotide sequences of the cDNAs encoding the core gene of 52 HCV isolates. These nucleotide sequences are shown in the sequence listing as SEQ ID NO:103 through SEQ ID NO:154.

The core cDNAs of the present invention were obtained as follows. Viral RNA was extracted from serum and reversed transcribed as described above for cloning of the E1 cDNAs. The core cDNAs of the present invention were then amplified by polymerase chain reaction using primers deduced from previously determined sequences that flank the core gene (Bukh et al. (1992)) Proc. Natl. Acad. Sci. U.S.A., 89: 4942-4946; Bukh et al. (1993) Proc. Natl. Acad. Sci. U.S.A., 90: 8234-8238).

The deduced amino acid sequence of each of SEQ ID NO:103 through SEQ ID NO:154 are presented in the sequence listing as SEQ ID NO:155 through SEQ ID NO:206 where the amino acid sequence in SEQ ID NO:155 is deduced from the nucleotide sequence shown in SEQ ID NO:103, the amino acid sequence shown in SEQ ID NO:156 is deduced from the nucleotide sequence shown in SEQ ID NO:104 and so on. The deduced amino acid sequence of each of SEQ ID NOS: 155-206 starts at nucleotide 1 of the corresponding nucleotide sequence shown in SEQ ID NOS:103-154 and extends 572 nucleotides to a total length of 573 nucleotides.

Preferably, the E1 and core proteins and peptides of the present invention are substantially homologous to, and most preferably biologically equivalent to, native HCV E1 and core proteins and peptides. By "biologically equivalent" as used throughout the specification and claims, it is meant that the compositions are immunogenically equivalent to the native E1 and core proteins and peptides. The E1 and core proteins and peptides of the present invention may also stimulate the production of protective antibodies upon

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° injection into a mammal that would serve to protect the mammal upon challenge with HCV. By "substantially homologous" as used throughout the ensuing specification and claims to describe E1 and core proteins and peptides, it is meant a degree of homology in the amino acid
5 sequence of the E1 and core proteins and peptides to the native E1 and core proteins and peptides respectively. Preferably the degree of homology is in excess of 90, preferably in excess of 95, with a particularly preferred group of proteins being in excess of 99 homologous with
10 the native E1 or core proteins and peptides.

Variations are contemplated in the cDNA sequences shown in SEQ ID NO:1 through SEQ ID NO:51 and in SEQ ID NO:103 through SEQ ID NO:154 which will result in a nucleic acid sequence that is capable of directing
15 production of analogs of the corresponding protein shown in SEQ ID NO:52 through SEQ ID NO:102 and in SEQ ID NO:155 through SEQ ID NO:206. It should be noted that the cDNA sequences set forth above represent a preferred embodiment of the present invention. Due to the degeneracy of the
20 genetic code, it is to be understood that numerous choices of nucleotides may be made that will lead to a DNA sequence capable of directing production of the instant protein or its analogs. As such, DNA sequences which are functionally equivalent to the sequence set forth above or
25 which are functionally equivalent to sequences that would direct production of analogs of the E1 and core proteins produced pursuant to the amino acid sequences set forth above, are intended to be encompassed within the present invention.

30 The term analog as used throughout the specification or claims to describe the E1 and core proteins and peptides of the present invention, includes any protein or peptide having an amino acid residue sequence substantially identical to a sequence
35 specifically shown herein in which one or more residues

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° have been conservatively substituted with a biologically equivalent residue. Examples of conservative substitutions include the substitution of one polar (hydrophobic) residue such as isoleucine, valine, leucine or methionine for another, the substitution of one polar
5 (hydrophilic) residue for another such as between arginine and lysine, between glutamine and asparagine, between glycine and serine, the substitution of one basic residue such as lysine, arginine or histidine for another, or the substitution of one acidic residue, such as aspartic acid
10 or glutamic acid for another.

The phrase "conservative substitution" also includes the use of a chemically derivatized residue in place of a non-derivatized residue provided that the resulting protein or peptide is biologically equivalent to
15 the native E1 or core protein or peptide.

"Chemical derivative" refers to an E1 or core protein or peptide having one or more residues chemically derivatized by reaction of a functional side group. Examples of such derivatized molecules, include but are
20 not limited to, those molecules in which free amino groups have been derivatized to form amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or formyl groups. Free carboxyl groups may be derivatized to form
25 salts, methyl and ethyl esters or other types of esters or hydrazides. Free hydroxyl groups may be derivatized to form O-acyl or O-alkyl derivatives. The imidazole nitrogen of histidine may be derivatized to form N-imbenzylhistidine. Also included as chemical derivatives
30 are those proteins or peptides which contain one or more naturally-occurring amino acid derivatives of the twenty standard amino acids. For examples: 4-hydroxyproline may be substituted for proline; 5-hydroxylysine may be substituted for lysine; 3-methylhistidine may be
35 substituted for histidine; homoserine may be substituted

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° for serine; and ornithine may be substituted for lysine. The E1 and core proteins and peptide of the present invention also includes any protein or peptide having one or more additions and/or deletions of residues relative to the sequence of a peptide whose sequence is shown herein, so long as the peptide is biologically equivalent to the native E1 or core protein or peptide.

5 The present invention also includes a recombinant DNA method for the manufacture of HCV E1 and core proteins. In this method, natural or synthetic nucleic acid sequences may be used to direct the production of E1 and core proteins.

10 In one embodiment of the invention, the method comprises:

(a) preparation of a nucleic acid sequence capable of directing a host organism to produce HCV E1 or core protein;

(b) cloning the nucleic acid sequence into a vector capable of being transferred into and replicated in a host organism, such vector containing operational elements for the nucleic acid sequence;

(c) transferring the vector containing the nucleic acid and operational elements into a host organism capable of expressing the protein;

(d) culturing the host organism under conditions appropriate for amplification of the vector and expression of the protein; and

(e) harvesting the protein.

25 In another embodiment of the invention, the method for the recombinant DNA synthesis of an HCV E1 protein encoded by any one of the nucleic acid sequences shown in SEQ ID NOS:1-51 comprises:

(a) culturing a transformed or transfected host organism containing a nucleic acid sequence capable of directing the host organism to produce a protein, under conditions such that the protein is produced; said protein

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exhibiting substantial homology to a native E1 protein isolated from HCV having the amino acid sequence according to any one of the amino acid sequences shown in SEQ ID NOS:52-102 or combinations thereof.

In one embodiment, the RNA sequence of an HCV isolate was isolated and converted to cDNA as follows. Viral RNA is extracted from a biological sample collected from human subjects infected with hepatitis C and the viral RNA is then reverse transcribed and amplified by polymerase chain reaction using primers deduced from the sequence of HCV strain H-77 (Ogata et al. (1991)). Preferred primer sequences are shown as SEQ ID NOS:207-212 in the sequence listing. Once amplified, the PCR fragments are isolated by gel electrophoresis and sequenced.

In an alternative embodiment, the above method may be utilized for the recombinant DNA synthesis of an HCV core protein encoded by any one of the nucleic acid sequences shown in SEQ ID NOS: 103-154, where the protein produced by this method exhibits substantial homology to a native core protein isolated from HCV having amino acid sequence according to any one of the amino acid sequences shown in SEQ ID NOS: 155-206 or combinations thereof.

The vectors contemplated for use in the present invention include any vectors into which a nucleic acid sequence as described above can be inserted, along with any preferred or required operational elements, and which vector can then be subsequently transferred into a host organism and replicated in such organisms. Preferred vectors are those whose restriction sites have been well documented and which contain the operational elements preferred or required for transcription of the nucleic acid sequence.

The "operational elements" as discussed herein include at least one promoter, at least one operator, at least one leader sequence, at least one terminator codon,

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° and any other DNA sequences necessary or preferred for appropriate transcription and subsequent translation of the vector nucleic acid. In particular, it is contemplated that such vectors will contain at least one origin of replication recognized by the host organism
5 along with at least one selectable marker and at least one promoter sequence capable of initiating transcription of the nucleic acid sequence.

In construction of the recombinant expression vectors of the present invention, it should additionally
10 be noted that multiple copies of the nucleic acid sequence of interest (either E1 or core) and its attendant operational elements may be inserted into each vector. In such an embodiment, the host organism would produce greater amounts per vector of the desired E1 or core
15 protein. The number of multiple copies of the nucleic acid sequence which may be inserted into the vector is limited only by the ability of the resultant vector due to its size, to be transferred into and replicated and transcribed in an appropriate host microorganism.

20 Of course, those skilled in the art would readily understand that copies of both core and E1 nucleic acid sequence may be inserted into single vector such that a host organism transformed or transfected with said vector would produce both the desired E1 and core
25 proteins. For example, a polysistronic vector in which multiple different E1 and/or core proteins may be expressed from a single vector is created by placing expression of each protein under control of an internal ribosomal entry site (IRES) (Molla, A. et al. Nature,
30 356:255-257 (1992); Gong, S.K. et al. J. of Virol., 263:1651-1660 (1989)).

In another embodiment, restriction digest fragments containing a coding sequence for E1 or core proteins can be inserted into a suitable expression vector
35 that functions in prokaryotic or eukaryotic cells. By

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° suitable is meant that the vector is capable of carrying and expressing a complete nucleic acid sequence coding for an E1 or core protein. Preferred expression vectors are those that function in a eukaryotic cell. Examples of such vectors include but are not limited to vaccinia virus
5 vectors, adenovirus or herpes viruses. A preferred vector is the baculovirus transfer vector, pBlueBac.

In yet another embodiment, the selected recombinant expression vector may then be transfected into a suitable eukaryotic cell system for purposes of
10 expressing the recombinant protein. Such eukaryotic cell systems include but are not limited to cell lines such as HeLa, MRC-5 or CV-1. A preferred eukaryotic cell system is SF9 insect cells.

The expressed recombinant protein may be
15 detected by methods known in the art including, but not limited to, Coomassie blue staining and Western blotting.

The present invention also relates to substantially purified and isolated recombinant E1 and core proteins. In one embodiment, the recombinant protein
20 expressed by the SF9 cells can be obtained as a crude lysate or it can be purified by standard protein purification procedures known in the art which may include differential precipitation, molecular sieve chromatography, ion-exchange chromatography, isoelectric
25 focusing, gel electrophoresis and affinity and immunoaffinity chromatography. The recombinant protein may be purified by passage through a column containing a resin which has bound thereto antibodies specific for the open reading frame (ORF) protein.

30 The present invention further relates to the use of recombinant E1 and core proteins as diagnostic agents and vaccines. In one embodiment, the expressed recombinant proteins of this invention can be used in immunoassays for diagnosing or prognosing hepatitis C in a
35 mammal. For the purposes of the present invention,

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° "mammal" as used throughout the specification and claims, includes, but is not limited to humans, chimpanzees, other primates and the like. In a preferred embodiment, the immunoassay is useful in diagnosing hepatitis C infection in humans.

5 Immunoassays of the present invention may be those commonly used by those skilled in the art including, but not limited to, radioimmunoassay, Western blot assay, immunofluorescent assay, enzyme immunoassay, chemiluminescent assay, immunohistochemical assay, 10 immunoprecipitation and the like. Standard techniques known in the art for ELISA are described in Methods in Immunodiagnosis, 2nd Edition, Rose and Bigazzi, eds., John Wiley and Sons, 1980 and Campbell et al., Methods of Immunology, W.A. Benjamin, Inc., 1964, both of which are 15 incorporated herein by reference. Such assays may be a direct, indirect, competitive, or noncompetitive immunoassay as described in the art (Oellerich, M. 1984. J. Clin. Chem. Clin. BioChem 22:895-904) Biological samples appropriate for such detection assays include, but 20 are not limited to serum, liver, saliva, lymphocytes or other mononuclear cells.

 In a preferred embodiment, test serum is reacted with a solid phase reagent having surface-bound recombinant HCV E1 and/or core protein(s) as antigen(s). 25 The solid surface reagent can be prepared by known techniques for attaching protein to solid support material. These attachment methods include non-specific adsorption of the protein to the support or covalent attachment of the protein to a reactive group on the 30 support. After reaction of the antigen with anti-HCV antibody, unbound serum components are removed by washing and the antigen-antibody complex is reacted with a secondary antibody such as labelled anti-human antibody. The label may be an enzyme which is detected by incubating 35 the solid support in the presence of a suitable

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° fluorimetric or calorimetric reagent. Other detectable labels may also be used, such as radiolabels or colloidal gold, and the like.

The HCV E1 and/or core proteins and analogs thereof may be prepared in the form of a kit, alone, or in combinations with other reagents such as secondary antibodies, for use in immunoassays.

In yet another embodiment the recombinant E1 and core proteins or analogs thereof can be used as a vaccine to protect mammals against challenge with hepatitis C. The vaccine, which acts as an immunogen, may be a cell, cell lysate from cells transfected with a recombinant expression vector or a culture supernatant containing the expressed protein. Alternatively, the immunogen is a partially or substantially purified recombinant protein. In yet another embodiment, the immunogen may be a fusion protein comprising core protein and a second, non-core protein joined together such that the core portion of the fusion protein will aggregate and "trap" the second protein on the surface of the particle produced by aggregation of the core protein. (Molecular Biology of the Hepatitis B Virus", McLachlan, A. (1991) CRC Press, Boca Raton, Fla.). Alternatively, the core protein could be mixed with the second protein in vitro to produce particles in which all or part of the second protein was exposed on the surface of the particle. Such particles would then serve as a carrier in a multi-valent vaccine preparation. Second proteins or parts thereof which could be mixed with or fused to the core protein include, but are not limited to, HCV E1 and hepatitis B surface antigen.

While it is possible for the immunogen to be administered in a pure or substantially pure form, it is preferable to present it as a pharmaceutical composition, formulation or preparation.

The formulations of the present invention, both

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° for veterinary and for human use, comprise an immunogen as described above, together with one or more pharmaceutically acceptable carriers and optionally other therapeutic ingredients. The carrier(s) must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not deleterious to the recipient thereof. The formulations may conveniently be presented in unit dosage form and may be prepared by any method well-known in the pharmaceutical art.

10 All methods include the step of bringing into association the active ingredient with the carrier which constitutes one or more accessory ingredients. In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredient with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product into the desired formulation.

Formulations suitable for intravenous intramuscular, subcutaneous, or intraperitoneal administration conveniently comprise sterile aqueous solutions of the active ingredient with solutions which are preferably isotonic with the blood of the recipient. Such formulations may be conveniently prepared by dissolving the solid active ingredient in water containing physiologically compatible substances such as sodium chloride (e.g. 0.1-2.0M), glycine, and the like, and having a buffered pH compatible with physiological conditions to produce an aqueous solution, and rendering said solution sterile. These may be present in unit or multi-dose containers, for example, sealed ampules or vials.

The formulations of the present invention may incorporate a stabilizer. Illustrative stabilizers are preferably incorporated in an amount of 0.10-10,000 parts by weight per part by weight of immunogens. If two or

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more stabilizers are to be used, their total amount is preferably within the range specified above. These stabilizers are used in aqueous solutions at the appropriate concentration and pH. The specific osmotic pressure of such aqueous solutions is generally in the range of 0.1-3.0 osmoles, preferably in the range of 0.8-1.2. The pH of the aqueous solution is adjusted to be within the range of 5.0-9.0, preferably within the range of 6-8. In formulating the immunogen of the present invention, an anti-adsorption agent may be used.

Additional pharmaceutical methods may be employed to control the duration of action. Controlled release preparations may be achieved through the use of polymer to complex or adsorb the proteins or their derivatives. The controlled delivery may be exercised by selecting appropriate macromolecules (for example polyester, polyamino acids, polyvinyl pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine sulfate) and the concentration of macromolecules as well as the methods of incorporation in order to control release. Another possible method to control the duration of action by controlled-release preparations is to incorporate the proteins, protein analogs or their functional derivatives, into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly (methylmethacrylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions.

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When oral preparations are desired, the compositions may be combined with typical carriers, such as lactose, sucrose, starch, talc, magnesium stearate, crystalline cellulose, methyl cellulose, carboxymethyl cellulose, glycerin, sodium alginate or gum arabic among others.

The E1 and core proteins of the present invention may also be used as a delivery system for anti-virals to prevent or attenuate HCV infection in a mammal by utilizing the property of both proteins to self-aggregate in vitro to "trap" the antiviral within the particles produced via aggregation of the core and E1 proteins. Examples of anti-virals which could be delivered by such a system include, but are not limited to antisense DNA or RNAs.

Vaccination can be conducted by conventional methods. For example, the immunogen or immunogens (e.g. the E1 protein may be administered alone or in combination with the E1 proteins derived from other isolates of HCV) can be used in a suitable diluent such as saline or water, or complete or incomplete adjuvants. Further, the immunogen(s) may or may not be bound to a carrier to make the protein(s) immunogenic. Examples of such carrier molecules include but are not limited to bovine serum albumin (BSA), keyhole limpet hemocyanin (KLH), tetanus toxoid, and the like. The immunogen(s) can be administered by any route appropriate for antibody production such as intravenous, intraperitoneal, intramuscular, subcutaneous, and the like. The immunogen(s) may be administered once or at periodic intervals until a significant titer of anti-HCV antibody is produced. The antibody may be detected in the serum using an immunoassay.

In yet another embodiment, the immunogen may be nucleic acid sequence capable of directing host organism synthesis of E1 and/or core protein(s). Such nucleic acid

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° sequence may be inserted into a suitable expression vector by methods known to those skilled in the art. Expression vectors suitable for producing high efficiency gene transfer in vivo include retroviral, adenoviral and vaccinia viral vectors. Operational elements of such expression vectors are disclosed previously in the present specification and are known to one skilled in the art. Such expression vectors can be administered intravenously, intramuscularly, subcutaneously, intraperitoneally or orally.

10 In an alternative embodiment, direct gene transfer may be accomplished via intramuscular injection of, for example, plasmid-based eukaryotic expression vectors containing a nucleic acid sequence capable of directing host organism synthesis of E1 and/or core protein(s). Such an approach has previously been utilized to produce the hepatitis B surface antigen in vivo and resulted in an antibody response to the surface antigen (Davis, H.L. et al. (1993) Human molecular Genetics, 2:1847-1851; see also Davis et al. (1993) Human Gene Therapy, 4:151-159 and 733-740).

20 Doses of E1 and/or core protein(s)-encoding nucleic acid sequence effective to elicit a protective antibody response against HCV infection range from about 1 to about 500 μ g. A more preferred range being about 1 to about 500 μ g.

25 The E1 and/or core proteins and expression vectors containing a nucleic acid sequence capable of directing host organism synthesis of E1 and/or core protein(s) may be supplied in the form of a kit, alone, or in the form of a pharmaceutical composition as described above.

30 The administration of the immunogen(s) of the present invention may be for either a prophylactic or therapeutic purpose. When provided prophylactically, the immunogen(s) is provided in advance of any exposure to HCV

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° or in advance of any symptom of any symptoms due to HCV infection. The prophylactic administration of the immunogen serves to prevent or attenuate any subsequent infection of HCV in a mammal. When provided therapeutically, the immunogen(s) is provided at (or
5 shortly after) the onset of the infection or at the onset of any symptom of infection or disease caused by HCV. The therapeutic administration of the immunogen(s) serves to attenuate the infection or disease.

In addition to use as a vaccine, the
10 compositions can be used to prepare antibodies to HCV E1 and core proteins. The antibodies can be used directly as antiviral agents or they may be used in immunoassays disclosed herein to detect HCV E1 and core proteins present in patient sera.. To prepare antibodies, a host
15 animal is immunized using the E1 and/or core proteins native to the virus particle bound to a carrier as described above for vaccines. The host serum or plasma is collected following an appropriate time interval to provide a composition comprising antibodies reactive with
20 the E1 or core protein of the virus particle. The gamma globulin fraction or the IgG antibodies can be obtained, for example, by use of saturated ammonium sulfate or DEAE Sephadex, or other techniques known to those skilled in the art. The antibodies are substantially free of many of
25 the adverse side effects which may be associated with other anti-viral agents such as drugs.

The antibody compositions can be made even more compatible with the host system by minimizing potential adverse immune system responses. This is accomplished by
30 removing all or a portion of the Fc portion of a foreign species antibody or using an antibody of the same species as the host animal, for example, the use of antibodies from human/human hybridomas. Humanized antibodies (i.e., nonimmunogenic in a human) may be produced, for example,
35 by replacing an immunogenic portion of an antibody with a

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corresponding, but nonimmunogenic portion (i.e., chimeric antibodies). Such chimeric antibodies may contain the reactive or antigen-binding portion of an antibody from one species and the Fc portion of an antibody (nonimmunogenic) from a different species. Examples of chimeric antibodies, include but are not limited to, non-human mammal-human chimeras, rodent-human chimeras, murine-human and rat-human chimeras (Robinson et al., International Patent Application 184,187; Taniguchi M., European Patent Application 171,496; Morrison et al., European Patent Application 173,494; Neuberger et al., PCT Application WO 86/01533; Cabilly et al., 1987 Proc. Natl. Acad. Sci. USA 84:3439; Nishimura et al., 1987 Canc. Res. 47:999; Wood et al., 1985 Nature 314:446; Shaw et al., 1988 J. Natl. Cancer Inst. 80:15553, all incorporated herein by reference).

General reviews of "humanized" chimeric antibodies are provided by Morrison S., 1985 Science 229:1202 and by Oi et al., 1986 BioTechniques 4:214.

Suitable "humanized" antibodies can be alternatively produced by CDR or CEA substitution (Jones et al., 1986 Nature 321:552; Verhoeyan et al., 1988 Science 239:1534; Biedler et al. 1988 J. Immunol. 141:4053, all incorporated herein by reference).

The antibodies or antigen binding fragments may also be produced by genetic engineering. The technology for expression of both heavy and light chain genes in E. coli is the subject of the PCT patent applications; publication number WO 901443, WO901443, and WO 9014424 and in Huse et al., 1989 Science 246:1275-1281.

The antibodies can also be used as a means of enhancing the immune response. The antibodies can be administered in amount similar to those used for other therapeutic administrations of antibody. For example, normal immune globulin is administered at 0.02-0.1 ml/lb body weight during the early incubation period of other

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° viral diseases such as rabies, measles, and hepatitis B to interfere with viral entry into cells. Thus, antibodies reactive with the HCV E1 and/or core proteins can be passively administered alone or in conjunction with another anti-viral agent to a host infected with an HCV to enhance the immune response and/or the effectiveness of an antiviral drug.

Alternatively, anti-HCV E1 antibodies and anti-HCV core antibodies can be induced by administered anti-idiotypic antibodies as immunogens. Conveniently, a purified anti-HCV E1 or anti-HCV core antibody preparation prepared as described above is used to induce anti-idiotypic antibody in a host animal, the composition is administered to the host animal in a suitable diluent. Following administration, usually repeated administration, the host produces anti-idiotypic antibody. To eliminate an immunogenic response to the Fc region, antibodies produced by the same species as the host animal can be used or the Fc region of the administered antibodies can be removed. Following induction of anti-idiotypic antibody in the host animal, serum or plasma is removed to provide an antibody composition. The composition can be purified as described above for anti-HCV E1 and anti-HCV core antibodies, or by affinity chromatography using anti-HCV E1 or anti-HCV core antibodies bound to the affinity matrix. The anti-idiotypic antibodies produced are similar in conformation to the authentic HCV E1 or core protein and may be used to prepare an HCV vaccine rather than using an HCV E1 or core protein.

When used as a means of inducing anti-HCV virus antibodies in an animal, the manner of injecting the antibody is the same as for vaccination purposes, namely intramuscularly, intraperitoneally, subcutaneously or the like in an effective concentration in a physiologically suitable diluent with or without adjuvant. One or more booster injections may be desirable.

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The HCV E1 and core proteins of the invention are also intended for use in producing antiserum designed for pre- or post-exposure prophylaxis. Here an E1 or core protein, or mixture of E1 and/or core proteins is formulated with a suitable adjuvant and administered by injection to human volunteers, according to known methods for producing human antisera. Antibody response to the injected proteins is monitored, during a several-week period following immunization, by periodic serum sampling to detect the presence of anti-HCV E1 and/or anti-HCV core serum antibodies, using an immunoassay as described herein.

The antiserum from immunized individuals may be administered as a pre-exposure prophylactic measure for individuals who are at risk of contracting infection. The antiserum is also useful in treating an individual post-exposure, analogous to the use of high titer antiserum against hepatitis B virus for post-exposure prophylaxis.

For both in vivo use of antibodies to HCV virus-like particles and proteins and anti-idiotypic antibodies and diagnostic use, it may be preferable to use monoclonal antibodies. Monoclonal anti-HCV E1 and anti-HCV core protein antibodies or anti-idiotypic antibodies can be produced as follows. The spleen or lymphocytes from an immunized animal are removed and immortalized or used to prepare hybridomas by methods known to those skilled in the art. (Goding, J.W. 1983. Monoclonal Antibodies: Principles and Practice, Pladermic Press, Inc., NY, NY, pp. 56-97). To produce a human-human hybridoma, a human lymphocyte donor is selected. A donor known to be infected with HCV (where infection has been shown for example by the presence of anti-virus antibodies in the blood or by virus culture) may serve as a suitable lymphocyte donor. Lymphocytes can be isolated from a peripheral blood sample or spleen cells may be used if the donor is subject to splenectomy. Epstein-Barr virus (EBV)

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° can be used to immortalize human lymphocytes or a human fusion partner can be used to produce human-human hybridomas. Primary in vitro immunization with peptides can also be used in the generation of human monoclonal antibodies.

5 Antibodies secreted by the immortalized cells are screened to determine the clones that secrete antibodies of the desired specificity. For monoclonal anti-E1 and anti-core antibodies, the antibodies must bind to HCV E1 and core proteins respectively. For monoclonal
10 anti-idiotypic antibodies, the antibodies must bind to anti-E1 and anti-core protein antibodies respectively. Cells producing antibodies of the desired specificity are selected.

 The present invention also relates to the use of
15 single-stranded antisense poly- or oligonucleotides derived from nucleotide sequences substantially homologous to those shown in SEQ ID NOs:1-51 to inhibit the expression of hepatitis C E1 genes. The present invention further relates to the use of single-stranded anti-sense
20 poly- or oligo-nucleotides derived from nucleotide sequences substantially homologous to those shown in SEQ ID NOs:103-154 to inhibit the expression of hepatitis C core genes. Alternatively, the anti-sense poly- or oligo-nucleotides may be complementary to both the E1 and core
25 genes and hence, inhibit the expression of both hepatitis C E1 and core genes. By substantially homologous as used throughout the specification and claims to describe the nucleic acid sequences of the present invention, is meant a level of homology between the nucleic acid sequence and
30 the SEQ ID NOs. referred to in the above sentence. Preferably, the level of homology is in excess of 80%, more preferably in excess of 90%, with a preferred nucleic acid sequence being in excess of 95% homologous with the DNA sequence shown in the indicated SEQ ID NO. These
35 anti-sense poly- or oligonucleotides can be either DNA or

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RNA. The targeted sequence is typically messenger RNA and more preferably, a single sequence required for processing or translation of the RNA. The anti-sense poly- or oligonucleotides can be conjugated to a polycation such as polylysine as disclosed in Lemaitre, M. et al. ((1989) Proc. Natl. Acad. Sci. USA 84:648-652) and this conjugate can be administered to a mammal in an amount sufficient to hybridize to and inhibit the function of the messenger RNA.

The present invention further relates to multiple computer-generated alignments of the nucleotide and deduced amino acid sequences shown in SEQ ID NOS:1-206. Computer analysis of the nucleotide sequences shown in SEQ ID NOS:1-51 and 103-154 and of the deduced amino acid sequences shown in SEQ ID NOS:52-102 and 155-206 can be carried out using commercially available computer programs known to one skilled in the art.

In one embodiment, computer analysis of SEQ ID NOS:1-51 by the program GENALIGN (Intelligenetics, Inc. Mountainview, CA) results in distribution of the 51 HCV E1 sequences into twelve genotypes based upon the degree of variation of the sequences. For the purposes of the present invention, the nucleotide sequence identity of E1 cDNAs of HCV isolates of the same genotype is in the range of about 85% to about 100% whereas the identity of E1 cDNA sequences of different genotypes is in the range of about 50% to about 80%.

The grouping of SEQ ID NOS:1-51 into twelve HCV genotypes is shown below.

	<u>SEQ ID NOS:</u>	<u>Genotypes</u>
30	1-8	I/1a
	9-25	II/1b
	26-29	III/2a
	30-33	IV/2b
	34	2c
	35-39	V/3a
	40	4a
35	41	4b

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42-43	4c
44	4d
45-50	5a
51	6a

For those genotypes containing more than one E1 nucleotide sequence, computer alignment of the constituent nucleotide sequences of the genotype was conducted using GENALIGN in order to produce a consensus sequence for each genotype. These alignments and their resultant consensus sequences are shown in Figures 1A-1 thru 1G-5 for the seven genotypes (I/1a, II/1b, III/2a, IV/2b, V/3a, 4c and 5a) which comprise more than one nucleotide sequence.

Further alignment of the consensus sequences of Figures 1A-1 thru 1G-5 with SEQ ID NO:34 (genotype 2c), SEQ ID NO:40 (genotype 4a), SEQ ID NO:41 (genotype 4b), SEQ ID NO:44 (genotype 4d) and SEQ ID NO:51 (genotype 6a) produces a consensus sequence for all twelve genotypes as shown in Figures 1H-1 thru 1H-5. The multiple alignments of nucleotide sequences shown in Figures 1A-1 thru 1H-5 produce consensus sequences which serve to highlight regions of homology and non-homology between sequences found within the same genotype or in different genotypes and hence, these alignments can be used by one skilled in the art to design oligonucleotides useful as reagents in diagnostic assays for HCV.

Examples of purified and isolated oligonucleotide sequences derived from the consensus sequences shown in Figures 1A-1 thru 1H-5 include, but are not limited to, SEQ ID NOs:213-239 where these oligonucleotides are useful as "genotype-specific" primers and probes since these oligonucleotides can hybridize specifically to the nucleotide sequence of the E1 gene of HCV isolates belonging to a single genotype. The genotype-specificity of the oligonucleotides shown in SEQ ID NOs:213-239 is as follows: SEQ ID NOs:213-214 are specific for genotype I/1a; SEQ ID NOs:215-216 are

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specific for genotype II/1b; SEQ ID NOs:217-218 are specific for genotype III/2a; SEQ ID NOs:219-220 are specific for genotype IV/2b; SEQ ID NOs:221-223 are specific for genotype 2c; SEQ ID NOs:224-226 are specific for genotype V/3a; SEQ ID NOs:227-228 are specific for genotype 4a; SEQ ID NOs:229-230 are specific for genotype 4b; SEQ ID NOs:231-232 are specific for genotype 4c; SEQ ID NOs:233-234 are specific for genotype 4d; SEQ ID NOs:235-236 are specific for genotype 5a and SEQ ID NOs:237-239 are specific for genotype 6a.

In another embodiment, the computer analysis of SEQ ID NOs:103-154 by the program GENALIGN results in distribution of the 52 HCV core sequences into 14 genotypes based upon the degree of variation of the sequences.

The grouping of SEQ ID NOs:103-154 into 14 HCV genotypes is shown below.

	<u>SEQ ID NOs:</u>	<u>Genotypes</u>
	103-108	I/1a
	109-124	II/1b
	125-128	III/2a
	129-133	IV/2b
	134	2c
	135-138	V/3a
	139	4a
	141	4b
	143	4c
	144	4c
	145	4d
	142	4e
	140	4f
	146-153	5a
	154	6a

These 14 genotypes can be further grouped into 6 major genotypes designated genotypes 1-6 where genotype 1 comprises the sequences contained in minor genotypes I/1a and II/1b; genotype 2 comprises the sequences contained in minor genotypes III/2a, IV/2b and 2c; genotype 3 comprises sequences contained in genotype V/3a; genotype 4 comprises

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sequences contained in minor genotypes 4a-4f; genotype 5 comprises the sequences contained in genotype 5a and genotype 6 comprises the sequence contained in genotype 6a. Computer alignment of the constituent nucleotide sequences of the core cDNAs falling within genotypes I/1a, II/1b, III/2a, IV/2b, V/3a and 5a, to produce a consensus sequence for each of these genotypes is shown in Figures 6A-1 thru 6A-4 (I/1a), 6B-1 thru 6B-10 (II/1b), 6D-1 thru 6D-3 (III/2a), 6E-1 thru 6E-4 (IV/2b), 6G-1 thru 6G-3 (V/3a) and 6I-1 thru 6I-4 (5a). The alignment of the sequences found in minor genotypes I/1a and II/1b to produce a consensus sequence for major genotype 1 is shown in Figures 6C-1 thru 6C-10. The alignment of the sequences contained in minor genotypes III/2a, IV/2b and 2c to produce a consensus sequence for major genotype 2 is shown in Figures 6F-1 thru 6F-5. The alignment of the nucleotide sequences contained in minor genotypes 4a-4f to produce a consensus sequence for major genotype 4 is shown in Figures 6H-1 thru 6H-4. Further alignment of the consensus sequences shown in Figures 6C-1 thru 6C-10, 6F-1 thru 6F-5, 6G-1 thru 6G-3, 6H-1 thru 6H-4 and 6I-1 thru 6I-4 with SEQ ID NO:154 (genotype 6a/major genotype 6) to produce a consensus sequence for all genotypes is shown in Figures 6J-1 thru 6J-4 and alignment of the consensus sequences shown in Figures 6A-1 thru 6A-4, 6B-1 thru 6B-10, 6D-1 thru 6D-3, 6E-1 thru 6E-4, 6G-1 thru 6G-3 and 6I-1 thru 6I-4 with SEQ ID NO:139 (genotype 4a), SEQ ID NO:141 (genotype 4b), SEQ ID NO:143 (genotype 4c), SEQ ID NO:145 (genotype 4d), SEQ ID NO:142 (genotype 4e), SEQ ID NO:140 (genotype 4f) and SEQ ID NO:154 (genotype 6a) to produce a consensus sequence for all fourteen genotypes is shown in Figures 6K-1 and 6K-2. As with the alignments of the envelope (E1) nucleotide sequences, the consensus sequences shown in Figures 6A-1 thru 6K-2 serve to highlight regions of homology and non-homology between sequences found within the same genotype or in different

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- ° genotypes and hence, can be used by one skilled in the art to design oligonucleotides useful as reagents in diagnostic assays for HCV.

- For example, purified and isolated oligonucleotide sequences derived from the consensus sequences shown in Figures 6A-1 thru 6K-2 may be useful as genotype-specific primers and probes since these oligonucleotides can hybridize specifically to the nucleotide sequence of the core gene of HCV isolates belonging to a given genotype. Examples of regions of the consensus sequence of the core gene of a given genotype from which primers specific for that genotype may be deduced include but are not limited to, the nucleotide domains shown below for each genotype. The sequence in which the indicated nucleotide domains are found are indicated in parentheses to the right of each genotype.
- 15 Genotype 1 (Consensus Sequence of Figures 6C-1 thru 6C-10)
427-466, 444-483, 447-486 (5'-3', sense)
505-466, 522-483, 525-486 (5'-3', antisense)
- 20 Genotype 1a (Consensus Sequence of Figures 6A-1 thru 6A-4)
141-180, 279-318 (5'-3', sense)
219-180, 246-207 (5'-3', antisense)
- 25 Genotype 1b (Consensus Sequence of Figures 6B-1 thru 6B-10)
67-106, 127-186, 234-273 (5'-3', sense)
144-106, 225-186, 311-272, 312-273 (5'-3', antisense)
- 30 Genotype 2 (Consensus Sequence of Figures 6F-1 thru 6F-5)
153-192, 162-201, 164-203, 168-207, 171-210, 182-221, 192-231, 193-232, 302-341 (5'-3', sense)
231-192, 240-201, 242-203, 246-207, 249-210, 260-221, 270-231, 271-232, 380-341 (5'-3', antisense)
- 35 Genotype III/2a (Consensus Sequence of Figures 6D-1 thru

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°

6D-3)

276-315, 306-355 (5'-3', sense)

309-270, 354-315, 394-355, 571-532 (5'-3', antisense)

5

Genotype IV/2b (Consensus Sequence of Figures 6E-1 thru 6E-4)

6-45, 135-174, 177-216, 309-348, 337-376, 375-414, 501-540 (5'-3', sense)

84-45, 213-174, 255-216, 387-348, 415-376, 453-414, 571-532, 573-540 (5'-3', antisense)

10

Genotype 2c (SEQ ID NO:134)

194-233, 273-312, 279-318, 417-456, 423-462, 504-543, 505-544, 517-556 (5'-3', sense)

15

272-233, 351-312, 354-315, 357-318, 450-411, 495-456, 501-462, 573-543, 556-573 (5'-3', antisense)

Genotype 3 or Genotype V/3a (Consensus Sequence of Figures 6G-1 thru 6G-3)

20

8-47, 45-84, 68-107, 87-126, 88-127, 90-129, 111-150, 142-181, 173-212, 177-216, 261-300, 276-315, 452-491, 520-559, 521-560, 529-568, 532-571, 533-572. (5'-3', sense)

25

86-47, 123-84, 146-107, 165-126, 186-147, 189-150, 219-180, 250-211, 251-212, 255-216, 339-300, 530-491, 573-543, 573-557, 573-559, 573-560. (5'-3', antisense)

Genotype 4 (Consensus Sequence of Figures 6H-1 thru 6H-4)

30

20-59 (5'-3', sense)
97-58, 98-59 (5'-3', antisense)Genotype 4a (SEQ ID NO:139)

35

111-150, 150-189, 174-213, 183-222, 192-231, 261-300, 376-415, 396-435, 531-570 (5'-3', sense)
186-147, 252-213, 270-231, 339-300, 454-415 (5'-3',

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° antisense)

Genotype 4b (SEQ ID NO:141)27-66, 30-69, 106-145, 271-310, 433-472, 447-486, 453-492
(5'-3', sense)5 105-66, 183-144, 184-145, 345-306, 348-309, 349-310, 468-
429, 510-471, 522-483, 570-531 (5'-3', antisense)Genotype 4c (SEQ ID NO:143)

174-213, 180-219, 207-246, 231-270 (5'-3', sense)

10 249-210, 252-213, 258-219, 309-270, 504-465 (5'-3',
antisense)Genotype 4d (SEQ ID NO:145)

173-212, 188-327, 430-469 (5'-3', sense)

15 248-209, 249-210, 250-211, 251-212, 366-327, 508-469 (5'-
3', antisense)Genotype 4e (SEQ ID NO:142)

160-199, 267-306, 287-326, 288-327, 524-564 (5'-3', sense)

20 238-199, 345-306, 365-326, 216-177, 522-483 (5'-3',
antisense)Genotype 4f (SEQ ID NO:140)

18-57, 36-75, 228-267, 396-435 (5'-3', sense)

25 96-57, 114-75, 306-267 (5'-3', antisense)

Genotype 5 or 5a (Consensus Sequence of Figures 6I-1 thru
6I-4)30 176-215, 177-216, 181-220, 195-234, 221-260, 252-291, 255-
294, 396-435, 435-474, 447-486, 498-537 (5'-3', sense)
254-215, 299-260, 310-271, 330-291, 333-294, 354-315, 464-
425, 471-432, 483-444, 570-531 (5'-3', antisense)Genotype 6 or 6a (SEQ ID NO:154)

35 20-59, 136-175, 156-195, 159-198, 175-214, 185-224, 277-

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° 316, 278-317, 312-351, 348-387, 405-444, 406-445, 407-446,
408-447, 411-450, 432-471, 433-472, 435-474, 522-561 (5'-
3', sense).
98-59, 214-175, 234-195, 237-198, 253-214, 262-223, 263-
224, 354-315, 355-316, 382-343, 390-351, 426-387, 468-429,
5 483-444, 484-445, 485-446, 486-447, 489-450, 510-471, 511-
472, 513-474 (5'-3', antisense)

Such nucleotide domains may range from about 15
to about 100 bases in length with a more preferred range
being about 30 to about 60 bases in length.

10 In an alternative embodiment, universal primers
able to hybridize to the nucleotide sequences of the core
gene of HCV isolates belonging to all of the genotypes
disclosed herein may be deduced from universally conserved
nucleotide domains of the consensus sequence shown in
15 Figures 6J-1 thru 6K-2. Examples of such nucleotide
domains include, but are not limited to, those shown
below:

nucleotides 1-20, 1-25, 1-26, 1-27, 1-33, 50-89,
51-90, 52-91, 53-92, 61-100, 62-101, 77-116, 78-117, 79-
20 118, 80-119, 81-120, 82-121, 83-122, 84-123, 85-124, 86-
125, 97-136, 98-137, 99-138, 100-139, 101-140, 102-141,
329-368, 330-369, 331-370, 332-371, 354-393, 355-394, 356-
395, 362-401, 363-402, 364-403, 365-404, 369-408, 442-481,
443-482, 457-496, 458-497, 475-514, 476-515, 477-516 (5'-
25 3, sense); and

nucleotides 40-1, 41-2, 42-3, 43-4, 51-12, 52-
13, 55-16, 56-17, 57-18, 58-19, 61-22, 62-23, 63-24,
64-25, 70-31, 124-85, 125-86, 126-87, 127-88, 128-89, 129-
90, 136-97, 137-98, 138-99,
30 149-110, 150-111, 151-112, 152-113, 153-114, 154-115, 155-
116, 156-117, 157-118, 158-119, 159-120, 170-131, 171-132,
172-133, 173-134, 174-135, 175-136, 403-364, 405-365, 406-
366, 406-367, 430-391, 431-392, 432-393, 436-397, 437-398,
438-399, 439-400, 517-478, 518-479, 519-480, 532-493, 533-
35 494, 550-511, 551-512 (5'-3', antisense)

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Those skilled in the art would readily understand that the term "antisense" as used herein refers to primer sequences which are the complementary sequence of the indicated consensus sequence or SEQ ID NO:. Further, provided with the above examples of regions of the consensus sequences or indicated SEQ ID NOS: from which to deduce universal and genotype-specific primers, those skilled in the art would readily be able to select pairs of primers, one sense and one antisense, which would be useful in the detection of HCV genotypes via the PCR methods described herein.

In yet another embodiment, the sequences shown in SEQ ID NO.:103-154 and the resultant consensus sequences produced by alignment of these SEQ ID NOs as shown in Figures 6A-1 thru 6K-2 may also be useful in the design of hybridization probes specific for a given HCV genotype. Examples of nucleotide domains of the consensus sequence or SEQ ID NO of a given genotype from which genotype-specific hybridization probes may be deduced include, but are not limited to, those shown below where the sequence from which the domains are found is indicated in parentheses to the right of each genotype.

<u>Genotype</u>	<u>Position</u>
1a (Consensus sequence of Figures 6A-1 thru 6A-4)	50-85 155-205 207-277 281-333 429-477 530-573
1b (Consensus sequence of Figures 6B-1 thru 6B-10)	81-131 159-225 252-318 411-472 530-573
2a (Consensus sequence of Figures 6D-1 thru 6D-3)	35-75 200-276 290-340 330-380 410-472 530-573

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°	2b (Consensus sequence of Figures 6E-1 thru 6E-4)	20-70
		149-199
		191-241
		240-285
		261-318
		323-373
		351-401
5		389-439
		429-477
		530-573
	2c (SEQ ID NO:134)	208-258
		230-276
		290-345
10		411-460
		430-490
		530-573
	3a (Consensus sequence of Figures 6G-1 thru 6G-3)	1-50
		40-100
		100-160
		145-190
15		190-240
		275-325
		411-455
		466-516
		530-573
	4a (SEQ ID NO:139)	35-85
		145-195
20		200-250
		255-305
		341-390
		390-440
		530-573
	4b (SEQ ID NO:141)	35-85
25		120-170
		180-225
		230-275
		285-335
		405-455
		462-492
		530-573
30	4c (SEQ ID NO:143)	35-85
		190-246
		245-295
		282-318
		372-415
		440-480
		530-573
35	4d (SEQ ID NO:145)	35-85

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		187-237
		302-352
		405-455
		444-494
		530-573
5	4e (SEQ ID NO:142)	35-85
		57-84
		174-224
		230-275
		290-340
		422-472
		530-573
10	4f (SEQ ID NO:140)	35-85
		174-224
		242-292
		290-340
		422-472
		530-573
15	5a (Consensus sequence of Figures 6I-1 thru 6I-4)	180-234
		265-315
		315-355
		420-486
		530-573
20	6a (SEQ ID NO:154)	34-84
		150-200
		180-230
		230-290
		291-333
		341-395
		429-490
		530-573
25	1 (Consensus sequence of Figures 6C-1 thru 6C-10)	192-241
		435-495
	2 (Consensus sequence of Figures 6F-1 thru 6F-5)	186-240
		320-360
		440-475
30	4 (Consensus sequence of Figures 6H-1 thru 6H-4)	40-80
35	In yet another embodiment, universal hybridization probes may be derived from the consensus sequences shown in Figures 6J-1 thru 6K-2. Examples of nucleotide domains of the consensus sequences shown in Figures 6J-1 thru 6K-2 from which universal hybridization probes may be derived include, but are not limited to, 1-	

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33; 85-141; 364-408; 478-516.

The oligonucleotides of this invention can be synthesized using any of the known methods of oligonucleotide synthesis (e.g., the phosphodiester method of Agarwal et al. 1972, Agnew. Chem. Int. Ed. Engl. 11:451, the phosphotriester method of Hsiung et al. 1979, Nucleic Acids Res 6:1371, or the automated diethylphosphoramidite method of Baeucage et al. 1981, Tetrahedron Letters 22:1859-1862), or they can be isolated fragments of naturally occurring or cloned DNA. In addition, those skilled in the art would be aware that oligonucleotides can be synthesized by automated instruments sold by a variety of manufacturers or can be commercially custom ordered and prepared. In a preferred embodiment, the oligonucleotides of the present invention are synthetic oligonucleotides. The oligonucleotides of the present invention may range from about 15 to about 100 nucleotides; with the preferred sizes being about 20 to about 60 nucleotides; a more preferred size being about 25 to about 50 nucleotides; and a most preferred size being about 30 to about 40 nucleotides.

The present invention also relates to methods for detecting the presence of HCV in a mammal, said methods comprising analyzing the RNA of a mammal for the presence of hepatitis C virus.

The RNA to be analyzed can be isolated from serum, liver, saliva, lymphocytes or other mononuclear cells as viral RNA, whole cell RNA or as poly(A)⁺ RNA. Whole cell RNA can be isolated by methods known to those skilled in the art. Such methods include extraction of RNA by differential precipitation (Birnbiom, H.C. (1988) Nucleic Acids Res., 16:1487-1497), extraction of RNA by organic solvents (Chomczynski, P. et al. (1987) Anal. Biochem., 162:156-159) and extraction of RNA with strong denaturants (Chirgwin, J.M. et al. (1979) Biochemistry, 18:5294-5299). Poly(A)⁺ RNA can be selected from whole

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cell RNA by affinity chromatography on oligo-d(T) columns (Aviv, H. et al. (1972) Proc. Natl. Acad. Sci., 69:1408-1412). A preferred method of isolating RNA is extraction of viral RNA by the guanidinium-phenol-chloroform method of Bukh et al. (1992a).

5 The methods for analyzing the RNA for the presence of HCV include Northern blotting (Alwine, J.C. et al. (1977) Proc. Natl. Acad. Sci., 74:5350-5354), dot and slot hybridization (Kafatos, F.C. et al. (1979) Nucleic Acids Res., 7:1541-1522), filter hybridization (Hollander, M.C. et al. (1990) Biotechniques; 9:174-179), RNase protection (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Press, Plainview, NY) and reverse-transcription polymerase chain reaction (RT-PCR) (Watson, J.D. et al. (1992) in "Recombinant DNA" Second Edition, W.H. Freeman and Company, New York).

A preferred method for analyzing the RNA is RT-PCR. In this method, the RNA can be reverse transcribed to first strand cDNA using a primer or primers derived from the nucleotide sequences shown in SEQ ID NOs:1-51 or SEQ ID NOs:103-154 or sequences complementary to those described. Once the cDNAs are synthesized, PCR amplification is carried out using pairs of primers designed to hybridize with sequences in the HCV E1 or core cDNA which are an appropriate distance apart (at least about 50 nucleotides) to permit amplification of the cDNA and subsequent detection of the amplification product. Alternatively, one can amplify both E1 and core cDNA sequences by using a primer pair where one primer hybridizes with the E1 cDNA sequence and the other primer hybridizes with the core cDNA sequence. Each primer of a pair is a single-stranded oligonucleotide of about 20 to about 60 bases in length with a more preferred range being about 30 to about 50 bases in length where one primer (the "upstream" primer) is complementary to the original RNA

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° and the second primer (the "downstream" primer) is complementary to the first strand of cDNA generated by reverse transcription of the RNA. The target sequence is generally about 100 to about 300 base pairs long but can be as large as 500-1500 base pairs. Optimization of the
5 amplification reaction to obtain sufficiently specific hybridization to the nucleotide sequence of interest (either E1 or core or both E1 and core) is well within the skill in the art and is preferably achieved by adjusting the annealing temperature.

10 In one embodiment, the primer pairs selected to amplify E1 and core cDNAs are universal primers. By "universal", as used to describe primers throughout the claims and specification, is meant those primer pairs which can amplify E1 and/or core gene fragments derived
15 from an HCV isolate belonging to any one of the genotypes of HCV described herein. Purified and isolated universal primers for E1 cDNAs are used in Example 1 of the present invention and are shown as SEQ ID NOS:207-212 where SEQ ID NOS:207 and 208 represent one pair of primers, SEQ ID
20 NOS:209 and 210 represent a second pair of primers and SEQ ID NOS:211-212 represent a third pair of primers. Nucleotide domains of the consensus sequence shown in Figures 6J-1 thru 6J-4 from which universal primers for core cDNAs may be deduced have previously been disclosed
25 within the present specification. Alternatively, a universal primer for E1 cDNA sequence and a universal primer for core cDNA sequence may be used as a universal primer pair to amplify both E1 and core cDNAs.

30 In an alternative embodiment, primer pairs selected to amplify E1 and/or core cDNAs are genotype-specific primers. In the present invention, genotype-specific primer pairs can readily be derived from the following genotype-specific E1 nucleotide domains: nucleotides 197-238 and 450-480 of the consensus sequence
35 of genotype I/1a shown in Figures 1A-1 and 1A-4;

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° nucleotides 197-238 and 450-480 of the consensus sequence of genotype II/1b shown in Figures 1B-4 and 1B-8;
nucleotides 199-238 and 438-480 of the consensus sequence of genotype III/2a shown in Figures 1C-2 and 1C-4;
nucleotides 124-177 and 450-480 of the consensus sequence
5 of genotype IV/2b shown in Figures 1D-2 and 1D-4;
nucleotides 124-177, 193-238 and 436-480 of SEQ ID NO:34 (genotype 2C); nucleotides 168-207, 294-339 and 406-480 of the consensus sequence of genotype V/3a shown in Figures 1E-2, 1E-3 and 1E-4; nucleotides 145-183 and 439-480 of
10 SEQ ID NO:40 (genotype 4a); nucleotides 168-207 and 432-480 of SEQ ID NO:41 (genotype 4b); nucleotides 130-183 and 450-480 of the consensus sequence of genotype 4c shown in Figures 1F-1 and 1F-2; nucleotides 130-183 and 450-480 of SEQ ID NO:44 (genotype 4d); nucleotides 166-208 and 437-
15 480 of the consensus sequence of genotype 5a shown in Figures 1G-2 and 1G-4 and nucleotides 168-207, 216-252 and 429-480 of SEQ ID NO:51 (genotype 6a). Genotype-specific HCV core nucleotide domains from which genotype-specific primers may be deduced have previously been described
20 herein. Those skilled in the art would readily appreciate that in a pair of genotype-specific primers, each primer is derived from different nucleotide domains specific for a given genotype. Also, it is understood by those skilled in the art that each pair of primers comprises one primer
25 which is complementary to the original viral RNA and the other which is complementary to the first strand of cDNA generated by reverse transcription of the viral RNA. For example, in a pair of genotype-specific primers for
30 genotype 4b, one primer would have a nucleotide sequence derived from region 168-207 of SEQ ID NO:40 and the other primer would have a nucleotide sequence which is the complement of region 432-480 of SEQ ID NO:40. One skilled in the art would readily recognize that such genotype-specific domains would also be useful in designing
35 oligonucleotides for use as genotype-specific

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- ° hybridization probes. Indeed, genotype-specific hybridization probes deduced from the E1 and core sequences of the present invention have been previously disclosed herein.

The amplification products of PCR can be detected either directly or indirectly. In one embodiment, direct detection of the amplification products is carried out via labelling of primer pairs. Labels suitable for labelling the primers of the present invention are known to one skilled in the art and include radioactive labels, biotin, avidin, enzymes and fluorescent molecules. The derived labels can be incorporated into the primers prior to performing the amplification reaction. A preferred labelling procedure utilizes radiolabeled ATP and T4 polynucleotide kinase (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Press, Plainview, NY). Alternatively, the desired label can be incorporated into the primer extension products during the amplification reaction in the form of one or more labelled dNTPs. In the present invention, the labelled amplified PCR products can be detected by agarose gel electrophoresis followed by ethidium bromide staining and visualization under ultraviolet light or via direct sequencing of the PCR-products. Thus, in one embodiment, the present invention relates to a method for determining the genotype of a hepatitis C virus present in a mammal where said method comprises: amplifying RNA of a mammal via RT-PCR using labelled genotype-specific primers for the amplification step of the cDNA produced by reverse transcription.

In yet another embodiment, unlabelled amplification products can be detected via hybridization with labelled nucleic acid probes radioactively labelled or, labelled with biotin, in methods known to one skilled in the art such as dot and slot blot hybridization

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(Kafatos, F.C. et al. (1979) or filter hybridization (Hollander, M.C. et al. (1990))).

In one embodiment, the nucleic acid sequences used as probes are selected from, and substantially homologous to, SEQ ID NOs:1-51 and/or SEQ ID NOs:103-154. Such probes are useful as universal probes in that they can detect PCR-amplification products of E1 and/or core cDNAs of an HCV isolate belonging to any of the HCV genotypes disclosed herein. The size of these probes can range from about 200 to about 500 nucleotides. In an alternative embodiment, the sequence alignments shown in Figures 1A-1 thru 1H-5 and 6A-1 thru 6J-4 may be used to design oligonucleotides useful as universal hybridization probes. Examples of core and envelope nucleotide domains from which such universal oligonucleotides may be deduced are disclosed herein.

In yet another embodiment, the present invention relates to a method for determining the genotype of a hepatitis C virus present in a mammal where said method comprises:

- (a) amplifying RNA of a mammal via RT-PCR to produce amplification products;
- (b) contacting said products with at least one genotype-specific oligonucleotide; and
- (c) detecting complexes of said products which bind to said oligonucleotide(s).

In this method, one embodiment of said amplification step is carried out using the universal primers for E1 or core cDNAs as disclosed above. In step (b) of this method, the genotype-specific sequences used as probes may be deduced from the genotype-specific E1 and core nucleotide domains disclosed herein. These probes are useful in specifically detecting PCR-amplification products of E1 or core cDNAs of HCV isolates belonging to one of the HCV genotypes disclosed herein. In a preferred embodiment, these probes are used alone or in combination

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° with other probes specific to the same genotype.

For example, a probe having a sequence according to SEQ ID NO:213 can be used alone or in combination with a probe having a sequence according to SEQ ID NO:214. The probes used in this method can range in size from about 15
5 to about 100 nucleotides with a more preferred range being about 30 to about 70 nucleotides. Such probes can be synthesized as described earlier.

In an alternative embodiment, the genotype of the amplification product of step (a) may be determined by
10 using the nucleic acid sequences shown in SEQ ID NOs: 1-51 and 103-154 as probes (Delwart, E. et al. (1993)) Science, 262: 1257-1261). Probes utilized in the method of Delwart et al. may range in size from about 100 to
15 about 1,000 nucleotides with a more preferred probe size being about 200 to about 800 base pairs and a most preferred probe size being about 300 to about 700 nucleotides.

The nucleic acid sequence used as a probe to detect PCR amplification products of the present invention
20 can be labeled in single-stranded or double-stranded form. Labelling of the nucleic acid sequence can be carried out by techniques known to one skilled in the art. Such labelling techniques can include radiolabels and enzymes (Sambrook, J. et al. (1989) in "Molecular Cloning, A
25 Laboratory Manual", Cold Spring Harbor Press, Plainview, New York). In addition, there are known non-radioactive techniques for signal amplification including methods for attaching chemical moieties to pyrimidine and purine rings (Dale, R.N.K. et al. (1973) Proc. Natl. Acad. Sci.,
30 70:2238-2242; Heck, R.F. (1968) S. Am. Chem. Soc., 90:5518-5523), methods which allow detection by chemiluminescence (Barton, S.K. et al. (1992) J. Am. Chem. Soc., 114:8736-8740) and methods utilizing biotinylated nucleic acid probes (Johnson, T.K. et al. (1983) Anal.
35 Biochem., 133:126-131; Erickson, P.F. et al. (1982) J. of

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Immunology Methods, 51:241-249; Matthaei, F.S. et al. (1986) Anal. Biochem., 157:123-128) and methods which allow detection by fluorescence using commercially available products.

The present invention also relates to computer analysis of the amino acid sequences shown in SEQ ID NOS:52-102 by the program GENALIGN. This analysis groups the 51 amino acid sequences shown in SEQ ID NOS:52-102 into twelve genotypes based upon the degree of variation of the amino acid sequences. For the purposes of the present invention, the amino acid sequence identity of E1 amino acid sequences of the same genotype ranges from about 85% to about 100% whereas the identity of E1 amino acid sequences of different genotypes ranges from about 45% to about 80%.

The grouping of SEQ ID NOS:52-102 into twelve HCV genotypes is shown below:

	<u>SEQ ID NOS:</u>	<u>Genotypes</u>
	52-59	I/1a
	60-76	II/1b
	77-80	III/2a
	81-84	IV/2b
	85	2c
	86-90	V/3a
	91	4a
	92	4b
	93-94	4c
	95	4d
	96-101	5a
	102	6a

For those genotypes containing more than one E1 amino acid sequence, computer alignment of the constituent sequences of each genotype was conducted using the computer program GENALIGN in order to produce a consensus sequence for each genotype. These alignments and their resultant consensus sequences are shown in Figures 2A-1 thru 2G-2 for the seven genotypes (I/1a, II/1b, III/2a, IV/2b, V/3a, 4c and 5a) which comprise more than one

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sequence. Further alignment of the consensus sequences shown in Figures 2A-1 thru 2G-2 with the amino acid sequences of SEQ ID NO:85 (genotype 2c); SEQ ID NO:91 (genotype 4a); SEQ ID NO:92 (genotype 4b); SEQ ID NO:95 (genotype 4d) and SEQ ID NO:102 (genotype 6a) to produce a consensus amino acid sequence for all twelve genotypes is shown in Figures 2H-1 and 2H-2. The multiple alignment of E1 amino acid sequences shown in Figures 2A-1 thru 2H-2 produces consensus sequences which serve to highlight regions of homology and non-homology between E1 amino acid sequences of the same genotype and of different genotypes and hence, these alignments can readily be used by those skilled in the art to design peptides useful in assays and vaccines for the diagnosis and prevention of HCV infection.

In another embodiment, the computer analysis of SEQ ID NOS: 155-206 by the probe genome results in distribution of the 52 HCV core sequences into 14 genotypes based upon identification of genotype-specific amino acid sequences.

The grouping of SEQ ID NOS: 155-206 into 14 HCV genotypes is shown below:

<u>SEQ ID NOS:</u>	<u>Genotypes</u>
155-160	I/1a
161-176	II/1b
177-180	III/2a
181-185	IV/2b
186	2c
187-190	V/3a
191	4a
193	4b
195	4c
196	4c
197	4d
194	4e
192	4f
198-205	5a
206	6a

These fourteen genotypes can be further grouped

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into six major genotypes designated genotypes 1-6 as described earlier for the core nucleotide sequences of the present application. Computer alignment of the amino acid sequences disclosed in SEQ ID NOS: 155-206 are shown in Figures 7A-1 thru 7J-1. As with the multiple alignments of the E-1 amino acid sequences, the consensus sequences shown in Figures 7A-1 thru 7J-1 serve to highlight regions of homology and nonhomology between core amino acid sequences of the same genotype and of different genotypes and hence, these alignments can readily be used by those skilled in the art to design peptides useful in assays and vaccines for the diagnosis and prevention of HCV infection.

Examples of purified and isolated peptides deduced from the alignments shown in Figures 2A-1 thru 2H-2 include, but are not limited to, SEQ ID NOS:240-263 wherein these peptides are derived from two regions of the amino acid sequences shown in Figures 2A-1 thru 2H-2, amino acids 48-80 and amino acids 138-160. The peptides shown in SEQ ID NOS. 240-263 are useful as genotype-specific diagnostic reagents since they are capable of detecting an immune response specific to HCV isolates belonging to a single genotype. The genotype-specificity of the peptides shown in SEQ ID NOS:240-263 are as follows: SEQ ID NOS:240 and 252 are specific for genotype IV/2b; SEQ ID NOS:241 and 253 are specific for genotype 2c; SEQ ID NOS:242 and 254 are specific for genotype III/2a; SEQ ID NOS:243 and 255 are specific for genotype V/a; SEQ ID NOS:244 and 256 are specific for genotype II/1b; SEQ ID NOS:245 and 257 are specific for genotype I/1a; SEQ ID NOS:246 and 258 are specific for genotype 4a; SEQ ID NOS:247 and 259 are specific for genotype 4c; SEQ ID NOS:248 and 260 are specific for genotype 4d; SEQ ID NOS:249 and 261 are specific for genotype 4b; SEQ ID NOS:250 and 262 are specific for genotype 5a and SEQ ID NOS:251 and 263 are specific for genotype 6a. In SEQ ID

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- ° NO:240, Xaa at position 22 is a residue of Ala or Thr, Xaa at position 24 is a residue of Val or Ile, Xaa at position 26 is a residue of Val or Met; in SEQ ID NO:242, Xaa at position 5 is a Ser or Thr residue, Xaa at position 11 is an Arg or Gln residue, Xaa at position 12 is an Arg or Gln residue; in SEQ ID NO:243, Xaa at position 3 is a Pro or Ser residue, Xaa at position 33 is a Leu or Met residue; in SEQ ID NO:244, Xaa at position 5 is a Thr or Ala residue, Xaa at position 13 is a Gly, Ala, Ser, Val or Thr residue, Xaa at position 14 is a Ser, Thr or Asn residue, Xaa at position 15 is a Val or Ile residue, Xaa at position 16 is a Pro or Ser residue, Xaa at position 18 is a Thr or Lys residue, Xaa at position 19 is a Thr or Ala residue, Xaa at position 22 is an Arg or His residue, Xaa at position 32 is an Ala, Val or Thr residue; in SEQ ID NO:245, Xaa at position 3 is an Ala or Pro residue, Xaa at position 4 is a Val or Met residue, Xaa at position 5 is a Thr or Ala residue, Xaa at position 17 is a Thr or Ala residue, Xaa at position 18 is a Thr or Ala residue, Xaa at position 23 is a His or Tyr residue; in SEQ ID NO:247, Xaa at position 10 is a Val or Ala residue, Xaa at position 11 is a Ser or Pro residue, Xaa at position 18 is an Asp or Glu residue Xaa at position 20 is a Leu or Ile residue; in SEQ ID NO:250, Xaa at position 3 is a Gln or His residue, Xaa at position 12 is an Asn, Ser or Thr residue, Xaa at position 13 is a Leu or Phe residue, Xaa at position 23 is an Ala or Val residue; in SEQ ID NO:252, Xaa at position 16 is a Val or Ala residue, Xaa at position 18 is a Glu or Gln residue; in SEQ ID NO:254, Xaa at position 2 is an Ala or Thr residue, Xaa at position 4 is a Met or Leu residue, Xaa at position 9 is an Ala or Val residue, Xaa at position 17 is an Ile or Leu residue, Xaa at position 20 is an Ile or Val residue, Xaa at position 21 is a Ser or Gly residue; in SEQ ID NO:151, Xaa at position 9 is a Val or Ile residue, Xaa at position 16 is a Leu or Val residue, Xaa at position 20 is an Ile or

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Leu residue; in SEQ ID NO:256, Xaa at position 2 is an Ala or Thr residue, Xaa at position 6 is a Val or Leu residue, Xaa at position 12 is an Ile or Leu residue, Xaa at position 16 is a Val or Ile residue, Xaa at position 17 is a Val, Leu or Met residue, Xaa at position 19 is a Met or Val residue, Xaa at position 21 is an Ala or Thr residue; in SEQ ID NO:257, Xaa at position 2 is a Thr or Ala residue, Xaa at position 6 is a Val, Ile or Met residue, Xaa at position 12 is an Ile or Val residue, Xaa at position 16 is a Ile or Val residue; in SEQ ID NO:155, Xaa at position 5 is a Leu or Val residue, Xaa at position 21 is a Thr or Ala residue; in SEQ ID NO:262, Xaa at position 1 is a Thr or Ala residue, Xaa at position 5 is a Val or Leu residue, Xaa at position 9 is a Leu, Met or Val residue, Xaa at position 23 is a Gly or Ala residue.

Examples of core amino acid domains from which genotype-specific peptides may be deduced, include but are not limited to, those shown below where the sequence in which the indicated domains are found is given in parentheses to the right of each genotype:

	<u>Genotype</u>	<u>Amino Acid Domains</u>
	1a (consensus sequence of Figures 7A-1 and 7A-2)	67-78
	1b (consensus sequence of Figures 7B-1 and 7B-2)	67-78
	2 (consensus sequence of Figures 7F-1 and 7F-2)	66-81
		110-119
25	2a (consensus sequence of Figure 7D-1)	67-78
	2b (consensus sequence of Figure 7E-1)	115-125
		67-78
	2c (SEQ ID NO:186)	123-133
		67-78
		75-81
		184-191
30	3a (consensus sequence of Figure 7G-1)	8-22
		32-46
		67-78
		158-170
		180-191
	4 (consensus sequence of Figures 7H-1 and 7H-2)	14-23
	4a (SEQ ID NO:191)	67-78
	4b (SEQ ID NO:193)	45-57
35	4c (SEQ ID NO:195)	67-78
		67-78

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°	4d	(SEQ ID NO:197)	67-78
	4e	(SEQ ID NO:194)	67-78
	4f	(SEQ ID NO:192)	67-78
	5a	(consensus sequence of Figure 7J-1)	67-78
	6a	(SEQ ID NO:206)	67-78
			101-108
			144-155
5			157-163

Those skilled in the art would be aware that the peptides of the present invention or analogs thereof can be synthesized by automated instruments sold by a variety of manufacturers or can be commercially custom-ordered and prepared. The term analog has been described earlier in the specification and for purposes of describing the peptides of the present invention, analogs can further include branched, cyclic or other non-linear arrangements of the peptide sequences of the present invention.

Alternatively, peptides can be expressed from nucleic acid sequences where such sequences can be DNA, cDNA, RNA or any variant thereof which is capable of directing protein synthesis. In one embodiment, restriction digest fragments containing a coding sequence for a peptide can be inserted into a suitable expression vector that functions in prokaryotic or eukaryotic cells. Such restriction digest fragments may be obtained from clones isolated from prokaryotic or eukaryotic sources which encode the peptide sequence.

Suitable expression vectors and methods of isolating clones encoding the peptide sequences of the present invention have previously been described. In yet another embodiment, an oligonucleotide capable of directing host organism synthesis of the given peptide may be synthesized and inserted into the expression vector.

The preferred size of the peptides of the present invention is from about 8 to about 100 amino acids in length when the peptides are chemically synthesized with a more preferred size being about 8 to about 30 amino acids and a most preferred size being about 10 to about 20

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° amino acids in length. For recombinantly expressed peptides, the size may range from about 20 to about 190 amino acids in length with a more preferred size being about 70 amino acids.

5 The present invention further relates to the use of genotype-specific peptides in methods of detecting antibodies against a specific genotype of HCV in biological samples. In one embodiment, at least one genotype-specific peptide deduced from a genotype-specific core or E1 amino acid domain may be used in any of
10 immunoassays described herein to detect antibodies specific for a single genotype of HCV. In another embodiment, at least one genotype-specific peptide deduced from a genotype-specific core nucleotide domain and at least one genotype-specific peptide deduced from an E1
15 amino acid domain may be used in an immunoassay to detect antibodies against a single genotype of HCV. A preferred immunoassay is ELISA.

It is understood by those skilled in the art that the diagnostic assays described herein using
20 genotype-specific oligonucleotides or genotype-specific peptides can be useful in assisting one skilled in the art to choose a course of therapy for the HCV-infected individual.

In an alternative embodiment, a mixture of
25 genotype-specific peptides can be used in an immunoassay to detect antibodies against multiple genotypes of HCV disclosed herein. For example, a mixture of genotype-specific peptides deduced from E1 amino acid sequences may comprise at least one peptide selected from SEQ ID
30 NOS:244-245 and 256-257; one peptide selected from SEQ ID NOS:240, 242, 252 and 254; one peptide selected from SEQ ID NOS:246-249 and 258-261; one peptide selected from SEQ ID NOS:250 and 262; one peptide selected from SEQ ID
35 NOS:243 and 255; one peptide selected from SEQ ID NOS:242 and 254 and one peptide selected from SEQ ID NOS:244 and

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263. In a preferred embodiment, the peptides of the present invention can be used in an ELISA assay as described previously for recombinant E1 and core proteins.

In an alternative embodiment, the peptide(s) utilized in an immunoassay to detect all the genotypes of HCV disclosed herein may be a universal peptide deduced from universally conserved amino acid domains of the E1 or core proteins disclosed herein.

Examples of universally conserved core amino acid domains within the consensus sequence shown in Figure 7J-1 from which universal peptides may be deduced include, but are not limited to amino acid domains 23-35, 53-66, 93-108, 122-138, 150-156, and 165-181 of the consensus sequence. Examples of universally conserved E1 amino acid domains within the HCV E1 protein are located within the consensus sequence for the 51 HCV E1 proteins shown in Figures 2H-1 and 2H-2 of the present application. Examples of universally conserved domains within the consensus sequence shown in Figures 2H-1 and 2H-2 include, but are not limited to, amino acid domains 10-20, 111-120, and 124-137 of the consensus sequence. The universal peptides of the present invention may be used in an immunoassay to detect antibodies in patient sera specific for any of the genotypes of HCV disclosed herein.

The peptides of the present invention or analogs thereof may be prepared in the form of a kit, alone or in combinations with other reagents such as secondary antibodies, for use in immunoassay.

In another embodiment, the genotype-specific and universal peptides of the present invention may be used to produce antibodies that will react against HCV E1 or core proteins in immunoassays. In one embodiment, a genotype-specific E1 or core peptide can be used alone or in combination with other E1 or core peptides specific to the same genotype as immunogens to produce antibodies specific to HCV proteins of a single genotype.

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In another embodiment, a mixture of peptides specific for different genotypes may be used to produce antibodies that will react with HCV proteins of any genotype disclosed herein. More preferably, antibodies reactive with HCV proteins of any genotype may be produced
5 by immunizing an animal with universal peptide(s) of the present invention. Examples of immunoassays in which such antibodies could be utilized to detect HCV E1 and core proteins in biological samples include, but are not limited to, radioimmunoassays and ELISAs. Examples of
10 biological samples in which HCV E1 and core proteins could be detected includes, but it is not limited to, serum, saliva and liver.

Of course, those skilled in the art would readily understand that the genotype-specific and
15 universal peptides of the present invention and expression vectors containing nucleic acid sequence capable of directing host organism synthesis of these peptides could also be used as vaccines against hepatitis C. Formulations suitable for administering the peptide(s) and
20 expression vectors of the present invention as immunogen, routes of administration, pharmaceutical compositions comprising the peptides expression vectors and so forth are the same as those previously described for recombinant E1 and core proteins.

25 The genotype-specific and universal peptides of the present invention and expression vectors containing nucleic acid sequence capable of direct host organism synthesis of these peptides may also be supplied in the form of a kit, alone, or in the form of a pharmaceutical
30 composition as described above for recombinant E1 and core proteins.

Any articles or patents referenced herein are incorporated by reference. The following examples illustrate various aspects of the invention but are in no
35 way intended to limit the scope thereof.

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MATERIALS

Serum used in these examples was obtained from 84 anti-HCV positive individuals who were previously found to be positive for HCV RNA in a cDNA PCR assay with primer set a from the 5' NC region of the HCV genome (Bukh, J. et al. (1992 (b)) Proc. Natl. Acad. Sci. USA 89:4942-4946). These samples were from 12 countries: Denmark (DK); Dominican Republic (DR); Germany (D); Hong Kong (HK); India (IND); Sardinia, Italy (S); Peru (P); South Africa (SA); Sweden (SW); Taiwan (T); United States (US); and Zaire (Z).

Example 1

Identification of the cDNA Sequence
of the E1 Gene of 51 Isolates of HCV via
RT-PCR Analysis of Viral RNA Using Universal Primers

Viral RNA was extracted from 100 μ l of serum by the guanidinium-phenol-chloroform method and the final RNA solution was divided into 10 equal aliquots and stored at -80°C as described (Bukh, et al. (1992 (a))). The sequences of the synthetic oligonucleotides used in the RT-PCR assay, deduced from the sequence of HCV strain H-77 (Ogata, N. et al. (1991) Proc. Natl. Acad. Sci. USA 88:3392-3396), are shown as SEQ ID NOS:207-212. One aliquot of the final RNA solution, equivalent to 10 μ l of serum, was used for cDNA synthesis that was performed in a 20 μ l reaction mixture using avian myeloblastosis virus reverse transcriptase (Promega, Madison, WI) and SEQ ID NO:208 as a primer. The resulting cDNA was amplified in a "nested" PCR assay by Taq DNA polymerase (Amplitaq, Perkin-Elmer/Cetus) as described previously (Bukh et al. (1992a)) with primer set e (SEQ ID NOS:207-210). Precautions were taken to avoid contamination with exogenous HCV nucleic acid (Bukh et al. 1992a)), and negative controls (normal, uninfected serum) were interspersed between every test sample in both the RNA

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extraction and cDNA PCR procedures. No false positive results were observed in the analysis. In most instances, amplified DNA (first or second PCR products) was reamplified with primers SEQ ID NO:211 and SEQ ID NO:212 prior to sequencing since these two primers contained EcoRI sites which would facilitate future cloning of the E1 gene. Amplified DNA was purified by gel electrophoresis followed by glass-milk extraction (Geneclean, BIO 101, LaJolla, CA) and both strands were sequenced directly by the dideoxynucleotide chain termination method (Bachman, B. et al. (1990) Nucl. Acids Res. 18:1309)) with phage T7 DNA polymerase (Sequenase, United States Biochemicals, Cleveland, OH), [alpha ³⁵S]dATP (Amersham, Arlington Heights, IL) or [alpha ³³P] dATP (Amersham or DuPont, Wilmington, DE) and sequencing primers. RNA extracted from serum containing HCV strain H-77, previously sequenced by Ogata, N. et al. (1991), was amplified with primer set e (SEQ ID NOS:207-210) and sequenced in parallel as a control. The nucleotide sequences of the envelope 1 (E1) gene of all 51 HCV isolates are shown as SEQ ID NOS:1 - 51. In all 51 HCV isolates, the E1 gene was exactly 576 nucleotides in length and did not have any in-frame stop codons.

Example 2

Computer Analysis of the Nucleotide and Deduced Amino Acid Sequences of the E1 Gene of 51 HCV Isolates

Multiple computer-generated alignments of the nucleotide (SEQ ID NOS:1-51, Figures 1A-1 thru 1H-5) and deduced amino acid sequences (SEQ ID NOS:52-102, Figures 2A-1 thru 2H-2) of the cDNAs of the 51 HCV isolates constructed using the computer program GENALIGN (Miller, R.H. et al. (1990) Proc. Natl. Acad. Sci. USA 87:2057-2061) resulted in the 51 HCV isolates being divided into twelve genotypes based upon the degree of variation of the

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° El gene sequence as shown in table 1.

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Biochemistry: Bukh *et al.*

Table 1. Percent nucleotide (nt) and amino acid (aa) sequence identity of the E1 gene among the 12 HCV genotypes.

	I/1a	II/1b	III/2a	IV/2b	2c	(V)/3a	4a	4b	4c	4d	5a	6a	nt:
	89.9-97.6	72.0-76.2	59.2-63.7	56.1-58.3	60.8-62.8	63.0-66.3	63.9-67.2	64.9-66.8	62.7-64.4	67.7-69.4	62.3-67.2	62.2-63.9	I/1a
aa:		88.9-97.9	58.3-62.2	53.8-57.5	60.1-61.5	63.9-67.2	60.9-63.7	63.4-65.8	61.6-65.1	63.0-65.5	62.2-66.5	61.6-63.0	II/1b
I/1a	91.1-98.4		88.0-91.3	69.1-71.0	72.7-73.6	58.0-60.8	61.5-62.7	58.9-60.4	59.7-63.4	58.7-61.3	56.6-60.8	55.0-56.8	III/2a
II/1b	75.5-80.7	90.1-97.9		92.7-95.0	67.5-68.9	56.3-58.3	58.9-60.8	56.4-57.6	57.1-59.9	57.5-59.0	53.5-56.6	53.6-55.2	IV/2b
III/2a	58.3-64.6	52.6-56.8	89.1-92.7		--	57.5-58.2	59.2	58.5	58.0-58.3	58.9	56.9-57.1	57.6	2c
IV/2b	54.2-56.8	51.0-54.2	69.3-72.9	93.8-96.4		93.8-99.1	64.4-65.3	62.7-64.1	60.9-62.5	62.3-63.9	61.8-64.4	58.0-58.9	(V)/3a
2c	56.3-60.4	52.6-55.7	74.5-77.1	67.7-69.8	--		--	74.8	75.5-78.0	74.8	62.8-64.6	62.0	4a
(V)/3a	64.1-68.8	66.7-70.8	54.7-58.9	54.2-56.8	52.1-53.6	94.3-98.4			74.0-74.8	72.0	63.9-64.6	62.7	4b
4a	69.3-73.4	64.6-67.2	62.0-63.0	58.9-60.4	58.3	66.1-68.8	--		90.1	77.6-78.6	62.7-64.8	63.0-64.4	4c
4b	66.7-69.3	66.1-70.3	53.6-56.3	52.1-53.1	53.6	62.0-64.6	76.0	--		--	64.4-66.1	64.1	4d
4c	66.1-72.9	64.6-69.3	55.2-61.5	54.2-58.3	54.7-58.3	63.0-65.6	77.1-81.3	79.2-80.2	89.6		90.1-95.7	60.6-63.2	5a
4d	73.4-75.5	66.7-70.3	56.3-58.9	55.2-55.7	54.2	63.5-64.6	78.1	77.6	82.8			--	6a
5a	66.1-73.4	64.1-70.3	52.6-57.3	50.5-53.1	54.2-56.3	60.4-64.1	67.2-68.2	65.1-67.2	67.7-71.4	69.3-71.4	92.7-97.4		
6a	64.6-65.6	62.5-65.6	49.0-51.0	49.0-50.5	50.5	57.8-58.9	66.1	62.5	66.1-67.2	66.7	62.0-63.5	--	

Nucleotide sequences analyzed in compiling the above table are shown in SEQ ID NOs:1-51 while the amino acid sequences analyzed are shown in SEQ ID NOs:52-102. The grouping of SEQ ID NOs: into genotypes is previously described in the specification.

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° The nucleotide and amino acid sequence identity of HCV isolates of the same genotype was in the range of 88.0-99.1% and 89.1-98.4%, respectively, whereas that of HCV isolates of different genotypes was in the range of 53.5-78.6% and 49.0-82.8%, respectively. The latter differences are similar to those found when comparing the envelope gene sequences of the various serotypes of the related flaviviruses, as well as other RNA viruses. When microheterogeneity in a sequence was observed, defined as more than one prominent nucleotide at a specific position, the nucleotide that was identical to that of the HCV prototype (HCV1, Choo et al. (1989)) was reported if possible. Alternatively, the nucleotide that was identical to the most closely related isolate is shown.

Analysis of the consensus sequence of the E1 protein of the 51 HCV isolates from this study demonstrated that a total of 60 (30.3%) of the 192 amino acids of the E1 protein were invariant among these isolates (Figures 3A and 3B). Most impressive, all 8 cysteine residues as well as 6 of 8 proline residues were invariant. The most abundant amino acids (e.g. alanine, valine and leucine) showed a very low degree of conservation. The consensus sequence of the E1 protein contained 5 potential N-linked glycosylation sites. Three sites at positions 209, 305 and 325 were maintained in all 51 HCV isolates. A site at position 196 was maintained in all isolates except the sole isolate of genotype 2c. Also, a site at position 234 was maintained in all isolates except one isolate of genotype I/1a, all four isolates of genotype IV/2b and the sole isolate of genotype 6a. Conversely, only genotype IV/2b isolates had a potential glycosylation site at position 233. Further analysis revealed a highly conserved amino acid domain (aa 302-328) in the E1 protein with 20 (74.1%) of 27 amino acids invariant among all 51 HCV isolates. It is possible that the 5' and 3' ends of this domain are conserved due to important cysteine residues and N-linked glycosylation

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- ° sites. The central sequence, 5'-GHRMAWDMM-3' (aa 315-323), may be conserved due to additional functional constraints on the protein structure. Finally, although the amino acid sequence surrounding the putative E1 protein cleavage site was variable, an amino acid doublet (GV) at position 380 was invariant among all HCV isolates.

A dendrogram of the genetic relatedness of the E1 protein of selected HCV isolates representing the 12 genotypes is shown in Fig. 4. This dendrogram was constructed using the program CLUSTAL (Higgins, D.G. et al. (1988) Gene, 73:237-244) and had a limit of 25 sequences. The scale showing percent identity was added based upon manual calculation. From the 51 HCV isolates for which the complete sequence of the E1 gene region was obtained, 25 isolates representing the twelve genotypes were selected for analysis. This dendrogram in combination with the analysis of the E1 gene sequence of 51 HCV isolates in Table 1 demonstrates extensive heterogeneity of this important gene.

The worldwide distribution of the 12 genotypes among 74 HCV isolates is depicted in Fig. 5. The complete E1 gene sequence was determined in 51 of these HCV isolates (SEQ ID NOS:1-51), including 8 isolates of genotype I/1a, 17 isolates of genotype II/1b and 26 isolates comprising genotypes III/2a, IV/2b, 2c, 3a, 4a-4d, 5a and 6a. In the remaining 23 isolates, all of genotypes I/1a and II/1b, the genotype assignment was based on a partial E1 gene sequence since they did not represent additional genotypes in any of the 12 countries. The number of isolates of a particular genotype is given in each of the 12 countries studied. Of the twelve genotypes, genotypes I/1a and II/1b were the most common accounting for 48 (65%) of the 74 isolates. Analysis of the E1 gene sequences available in the GenBank data base at the time of this study revealed that all 44 such sequences were of genotypes I/1a, II/1b, III/2a and IV/2b. Thus, based upon E1 gene analysis, 8 new genotypes

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- ° of HCV have been identified.

Also of interest, different HCV genotypes were frequently found in the same country, with the highest number of genotypes (five) being detected in Denmark. Of the twelve genotypes, genotypes I/1a, II/1b, III/2a, IV/2b and V/3a were widely distributed with genotype II/1b being identified in 11 of 12 countries studied (Zaire was the only exception). In addition, while genotypes I/1a and II/1b were predominant in the Americas, Europe and Asia, several new genotypes were predominant in Africa.

It was also found that genotypes I/1a, II/1b, III/2a, IV/2b and V/3a of HCV were widely distributed around the world, whereas genotypes 2c, 4a, 4b, 4d, 5a and 6a were identified only in discreet geographical regions. For example, the majority of isolates in South Africa comprised a new genotype (5a) and all isolates in Zaire comprised 3 new closely related genotypes (4a, 4b, 4c). These genotypes were not identified outside Africa.

Example 3

Identification of the cDNA Sequence Of The Core Gene Of 52 Isolates Of HCV

Viral RNA extraction, cDNA synthesis and "nested" PCR were carried out as in Example 1. For the cDNA PCR assay HCV-specific synthetic oligonucleotides deduced from previously determined sequences that flank the C gene were used. Amplified DNA was purified by gel electrophoresis followed by glass-milk extraction as described in Example 1 or by electroelution and both strands were sequenced directly. In 44 of the 52 HCV isolates studied the procedures for direct sequencing described in Example 1 were utilized. For a number of the HCV isolates confirmatory sequencing was performed with the Applied Biosystems 373A automated DNA sequencer and 8 HCV isolates of genotype I/1a or II/1b were sequenced exclusively by this method. All 73 negative control samples interspersed

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- ° among the test samples were negative for HCV RNA.

The amplified DNA fragment obtained in 50 of the 52 HCV isolates was specifically designed to overlap with previously obtained 5'NC sequences (Bukh et al. (1992b) Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946) and with the E1 sequences disclosed herein at approximately 80 nucleotide positions each. A complete match was observed in 6033 of 6035 overlapping nucleotides. Two discrepancies were observed in isolate US6 at nt 552 (C and T) and nt 561 (C and T) respectively. This may have been due to microheterogeneity at these nucleotide positions, since the remaining overlapping sequence was unique for isolate US6. In addition, there were 3 confirmed instances of microheterogeneity: nt 33 in isolate SA11 (C,T and T), nt 36 in isolate S45 (A,C and A), and nt 552 in isolate P10 (C,T and T). Overall, the excellent agreement in these overlapping sequences in this study with the NC sequences disclosed in Bukh et al. and with the E1 sequences disclosed herein definitively ruled out contamination as a source of non-authentic HCV sequences. Furthermore, this analysis proved that the sequences obtained were from a single population, and not from different populations as could happen in mixed infections.

The core (C) gene was exactly 573 nucleotides in length in all 52 HCV isolates with an amino terminal start codon and no in-frame stop codons. Microheterogeneity was observed in 26 of the 52 HCV isolates at 0.2-1.4% of the 573 nucleotide positions of the C gene, and resulted in changes in 0.5-1.0% of the 191 predicted amino acids in 12 of these isolates. A multiple sequence alignment was performed and it showed that the nucleotide identities of the C gene among these HCV isolates were in the range of 79.4-99.0%. In order to compare the genetic relatedness of HCV isolates in different gene regions, phylogenetic trees of the C gene of all 52 HCV isolates and the E1 gene of 51 HCV isolates were constructed using the unweighted pair-

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group method with arithmetic mean (Nei, M. (1987) Molecular Evolutionary Genetics (Columbia University Press, New York, N.Y., pp. 287-326) (Figures 8A and 8B). In both dendrograms a division of the 45 HCV isolates from which C and E1 genes had been cloned into at least six major genetic groups (genotypes 1-6) and 12 minor genetic groups (genotypes I/1a, II/1b, III/2a, IV/2b, 2c, V/3a, 4a-4d, 5a, and 6a) was observed. It is noteworthy that a major division in genetic distance between HCV isolates of genotype 2 and those of the other genotypes in the phylogenetic analyses of both gene sequences was observed. Furthermore, the divergence of the minor genotypes within genotype 2 exhibited a degree of heterogeneity that is equivalent to that observed among the major genotypes. Analysis of the C gene from isolates Z5 and Z8, which had a unique 5' NC sequence (Bukh et al. (1992)) but from which the E1 gene could not be amplified, revealed that these isolates represented two additional genotypes. The designations 4e and 4f are assigned to these genotypes that have not been described previously. Overall, the present specification demonstrates that the genetic relatedness of HCV isolates is equivalent when analyzing the most conserved gene (C) and one of the most variable genes (E1) of the HCV genome, thereby providing strong evidence for the suggested division into major and minor genotypes.

Example 4

Computer Analysis of the Nucleotide and Deduced Amino Acid Sequences Of The Core Gene Of 52 HCV Isolates

In order to study further the heterogeneity of the C gene, a consensus sequence of the core gene from the 52 HCV isolates (Figures 6J-1 thru 6J-4) was obtained. A total of 335 (58.5%) of the 573 nucleotides of the C gene were invariant among these HCV isolates. Nucleotides at the 1st and 2nd codon positions were invariant at 70.7% and 81.7% of these positions, respectively, while nucleotides

- 72 -

- ° at the 3rd position were invariant at only 23.0% of such positions. Stretches of 6 or more invariant nucleotides were observed from nucleotides 1-8, 22-27, 85-92, 110-125, 131-141, 334-340, 364-371, 397-404, and 511-516 and may be suitable for anchoring primers for amplification of HCV RNA in cDNA PCR assays.

Genotype-specific nucleotide positions of the core gene of hepatitis C virus were also noted for each of the genotypes. These genotype-specific nucleotides are shown below where each genotype-specific nucleotide is given in parentheses next to the nucleotide position in which it is found.

Genotype 1: 460 (C), 466 (C), 483 (C), 486 (G).

Genotype I/1a: 180 (T).

Genotype II/1b: 106 (C), 273 (G).

Genotype 2: 192 (C), 201 (A), 203 (A), 207 (G), 210 (C), 221 (A), 231 (A), 232 (A), 341 (A).

Genotype III/2a: 315 (C), 355 (G).

Genotype IV/2b: 45 (A), 174 (G), 216 (C), 348 (A), 376 (A), 414 (T).

Genotype 2c: 233 (G), 312 (C), 318 (A), 456 (C), 462 (G), 543 (C), 556 (T).

Genotype V/3a: 47 (T), 84 (A), 106 (G), 126 (A), 150 (T), 212 (G), 216 (A), 300 (A), 491 (T), 559 (C), 560 (A), 568 (G), 571 (A), 572 (G).

Genotype 4: 59 (T).

Genotype 4a: 213 (A), 231 (G), 415 (A).

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° Genotype 4b: 66 (G), 145 (G), 310 (A).

Genotype 4c: 213 (T), 219 (A), 270 (T).

Genotype 4d: 212 (T), 327 (G), 469 (C).

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Genotype 4e: 199 (C), 306 (A), 326 (A).

Genotype 4f: 57 (T), 75 (A), 267 (A).

10 Genotype 5a: 291 (G), 294 (C).

Genotype 6a: 59 (C), 175 (A), 195 (A), 198 (A), 214 (C),
224 (A), 316 (C), 351 (G), 387 (G), 444-447 (GGCT), 450
(G), 471-472 (AA), 474 (C).

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These genotype-specific nucleotides are of utility in designing the genotype-specific PCR primers and hybridization probes.

20 Finally, although the full length nucleic acid sequence of the C gene of isolates representing genotypes I/1a, II/1b, III/2a, IV/2b and V/3a have been reported by others, those of 9 of the 14 genotypes (i.e., 2c, 4a-4f, 5a and 6a) have not been reported previously. In sum, by aligning the consensus sequences of the major genotypes, the present application enables those skilled in the art to
25 map universally conserved sequences as well as genotype-specific sequences of the C gene among 14 genotypes of HCV.

In order to study the heterogeneity of the deduced C protein, a multiple sequence alignment of the predicted amino acids for all 52 HCV isolates was
30 performed, and a consensus sequence was obtained (Figure 7J-1). The identities of the predicted 191 amino acids of the C protein among these HCV isolates were in the range of 85.3-100.0%. A total of 132 (69.1%) of the 191 amino acids of the C protein were invariant. The most prevalent amino
35 acids in the consensus sequence were glycine (13.6%),

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arginine (12.6%), proline (11.0%), and leucine (9.9%). The most conserved amino acids were tryptophan (5 of 5 amino acids invariant), aspartic acid (5 of 5 amino acids invariant), proline (19 of 21 amino acids invariant) and glycine (23 of 26 amino acids invariant). Previous analyses indicated that HCV is evolutionarily related to pestiviruses (Miller et al. (1990) Proc. Natl. Acad. Sci. U.S.A. 87:2057-2061). In this regard, it is of interest to note that the C proteins of both viruses have a high content of proline residues (Collette M.S. et al. (1988) Virology 165:200-208), which are likely to be important in maintaining the structure of this protein. As is characteristic for a protein that binds to nucleic acid, the C protein has conserved amino acids that are basic and positively charged, and these are capable of neutralizing the negative charge of the HCV RNA encapsidated by this protein (Rice, C.M. et al. (1986) in *Togaviridae and Flaviviridae*, eds Schleinger, S. & Schlensinger, M.J. (Plenum Press, New York, N.Y.) pp. 279-326). Specifically, over 16% of the amino acids in the consensus sequence of the C protein of HCV are arginine and lysine that are located primarily in three clusters (i.e., from amino acids 6-23, 39-74 and 101-121) (Shih, C.M. et al. (1993) J. Gen. Virol. 67:5823-5832) (Figure 7J-1). The 10 arginine and lysine residues within amino acids 39-62 are invariant among all 52 HCV isolates, suggesting that this domain may represent an important RNA-binding site. The capsid proteins of the related flavi- and pestiviruses (Miller et al. (1990)) also have a high content of arginine and lysine (Rice et al. (1986); Collette et al. (1988)). Although there are three major hydrophilic regions (i.e., amino acids 2-23, 39-74 and 101-121) that are conserved in all 52 HCV isolates, the remainder of the C protein is hydrophobic. Interestingly, one such highly conserved hydrophobic domain from aa 24-39 is flanked by proline residues. The hydrophobic domains are likely to be

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- involved in protein-protein and/or protein-RNA interactions during assembly of the nucleocapsid, as well as in interaction with the lipoprotein envelope, as has been suggested for flaviviruses (Rice et al. (1986)). Other significant observations are: (i) a cluster of 5 invariant tryptophan residues from aa 76-107; (ii) the lack of an N-linked glycosylation site (N-X-T/S); (iii) two potential nuclear localization signals (i.e., PRRGPR at amino acids 38-43 and PRGRRQP at amino acids 58-64) that are present in all 52 HCV isolates (Shih et al. (1993)); and (iv) a putative DNA-binding motif SPRG at amino acids 99-102, found in 51 of the 52 HCV isolates, with SP present in all 52 isolates. This study demonstrates that the C protein has features that are highly conserved among the various genotypes of HCV, and that are known to be characteristic of capsid proteins of other related viruses.

It should also be noted that the phylogenetic analysis of the amino acid sequence of the C proteins was not capable of resolving the minor groups within genotypes 1 and 4 because of the conservation of this protein (data not shown). Indeed, only a few type-specific amino acids were identified. One striking example was that isolates of genotype 4 have an additional methionine at position 20 that is specific for this major genetic group. Finally, the conservation of the sequences surrounding the cleavage site between the C and the E1 proteins of the different genotypes, which has been determined to be between amino acid 191 (alanine) and aa 192 (tyrosine) in HCV isolates of genotype 1 was analyzed (Hijikata, M., et al. (1991) Proc. Natl. Acad. Sci. USA 88:5547-5551). The C-terminal sequence of C is serine-alanine in all but one of the 48 HCV isolates comprising genotypes 1, 2, 4, 5 and 6. However, all 4 HCV isolates of genotype 3 in this study, as well as isolates of genotype 3 published previously (Okamoto, H., et al. (1993) *J. Gen. Virol.* 74:2385-2390, Stuyver, L., et al. (1993) *Biochem. Biophys. Res. Comm.*

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- ° 192:635-641), contain alanine-serine at this position. Thus, studies will be needed to determine the C/E1 cleavage site in genotype 3 isolates. Overall, the present invention application discloses the mapping of universally conserved sequences, as well as genotype-specific sequences, of the C protein among 14 genotypes of HCV.

Implications of the mapping of universally conserved and genotype-specific core nucleotide and amino acid core sequences for diagnosis of HCV infection and for determination of HCV genotypes

- 10 Detection of antibodies directed against the HCV core protein is important in the diagnosis of HCV infection. The recombinant C22-3 protein, spanning amino acids 2-120 of the C gene, is a major component of the commercially available second-generation anti-HCV tests. Several studies have indicated that the three major hydrophilic regions of the C protein contain linear immunogenic epitopes (summarized in J. Clin. Microbiol., 30:1989-1994) (Sällberg, M. et al. (1992)). For example, antibodies against synthetic peptides from amino acids 1-18, 51-68 and 101-118 were detected in infected patients (Sällberg, M. et al. (1992)). The present application demonstrates that, while these immunogenic regions are highly conserved, genotype-specific differences are observed at several amino acid positions that may influence the specificity and sensitivity of the serological tests. One such example is that a single amino acid substitution at amino acid 110 has been demonstrated to affect seroreactivity (Sällberg, et al. (1992)). Despite the high degree of conservation in the immunodominant regions of the C protein among the different genotypes, it is possible that genetic heterogeneity of the C protein could lead to false negative results in current serological tests.

- 30 With respect to genotype analysis, several methods have been used to determine the genotype of HCV isolates without resorting to sequence analysis. These
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include PCR followed by: (i) amplification with type-specific primers (Okamoto, H. et al. (1992) J. Gen. Virol., 73:673-679); (ii) determination of restriction-length polymorphism (Simmons, P. et al. (1993) J. Gen. Virol., 74:661-668); and (iii) specific hybridization (Stuyver, L. (1993) J. Gen. Virol., 74:1093-1102). The proposed methods have primarily been based on 5' NC and C sequences. Previous studies suggested that 5' NC-based genotyping systems would only be predictive of the major genetic groups of HCV (Bukh, J., et al. (1992) Proc. Natl. Acad. Sci. USA 89:4942-4946, Bukh, J., et al. (1993) Proc. Natl. Acad. Sci. USA 90:8234-8238). The most widely used C-based genotype system has been the PCR assay with type-specific primers that was designed for distinguishing HCV isolates of genotypes I/1a, II/1b, III/2a, IV/2b and V/3a (Okamoto, H., et al. (1993) J. Gen. Virol. 74:2385-2390, Okamoto, H. et al. (1992) J. Gen. Virol. 73:673-679). Since this system was developed prior to the identification of genotypes 2c, 4a-4f, 5a and 6a there are significant limitations to this typing system. For example, the primers specific for genotype IV/2b (nt 270-251) are as highly conserved within isolates of genotype 4c and 6a as within the isolates of genotype IV/2b. Thus, this assay probably can not distinguish among these genotypes. Another C-based approach involves distinguishing between genotypes 1 and 2 by type-specific antibody responses (Machida et al (1992) Hepatology, 16:886-891). Synthetic peptides composed of amino acids 65-81 were found to be genotype-specific for genotypes 1 and 2 in ELISA assays. The present analysis of amino acid sequences demonstrated significant variation within isolates of genotypes 1 and 2. Thus it is likely that these peptides will not identify all isolates of genotypes 1 and 2. Furthermore, the peptide for genotype 1 was highly conserved within isolates of genotypes 3 and 4 and might detect antibodies against these genotypes as well. Finally, it should be pointed out that

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- most isolates of genotypes 3 and 4 had an identical amino acid sequence at positions 65-81.

Example 5

Detection by ELISA Based on Antigen from Insect Cells Expressing Complete E1 Or Core Protein

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Expression of E1 or Core protein in SF9 cells. A

cDNA (eg SEQ ID NO:1) encoding a complete E1 protein (eg SEQ ID NO:52) or a cDNA (eg SEQ ID NO:103) encoding a complete core protein (e.g. SEQ ID NO:155) is subcloned into pBlueBac - Transfer vector (Invitrogen) using standard subcloning procedures. The resultant recombinant expression vector is cotransfected into SF9 insect cells (Invitrogen) by the Ca precipitation method according to the Invitrogen protocol.

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ELISA Based on Infected SF9 cells. 5 x 10⁶ SF9

cells infected with the above-described recombinant expression vector are resuspended in 1 ml of 10 mM Tris-HCl, pH 7.5, 0.15M NaCl and are then frozen and thawed 3 times. 10 ul of this suspension is dissolved in 10 ml of carbonate buffer (pH 9.6) and used to cover one flexible microtiter assay plate (Falcon). Serum samples are diluted 1:20, 1:400 and 1:8000, or 1:100, 1:1000 and 1:10000. Blocking and washing solutions for use in the ELISA assay are PBS containing 10% fetal calf serum and 0.5% gelatin (blocking solution) and PBS with 0.05% Tween -20 (Sigma, St.Louis, MO) (washing solution). As a secondary antibody, peroxidase-conjugated goat IgG fraction to human IgG or horse radish peroxidase-labelled goat anti-Old or anti-New World monkey immunoglobulin is used. The results are determined by measuring the optical density (O.D.) at 405 nm.

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To determine if insect cells-derived E1 or core protein representing genotype I/a of HCV could detect anti-HCV antibody in chimpanzees infected with genotype I/1a of HCV, three infected chimpanzees are examined. The serum of

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- ° all 3 chimpanzees are found to seroconvert to anti-HCV.

Example 6

Use of the Complete E1 Protein as a Vaccine

5 Mammals are immunized with purified or partially purified E1 protein in an amount sufficient to stimulate the production of protective antibodies. The immunized mammals challenged with various genotypes of HCV are protected.

10 It is understood by one skilled in the art that the recombinant E1 protein used in the above vaccine can also be used in combination with other recombinant E1 proteins having an amino acid sequence shown in SEQ ID NOs:52-102. In addition, recombinant core proteins having
15 an amino acid sequence shown in SEQ ID NOs:155-206 could also be used in the above vaccine, either alone, in combination with other recombinant core proteins of the present invention, or in combination with recombinant E1 proteins having an amino acid sequence shown in SEQ ID
20 NOs:52-102.

Example 7

Determination of the Genotype of an HCV Isolate Via Hybridization of Genotype-Specific Oligonucleotides to RT-PCR Amplification Products.

25 Viral RNA is isolated from serum obtained from a mammal and is subjected to RT-PCR as in Example 1 or Example 3. Following amplification, the amplified DNA is purified as described in Example 1 or Example 3 and
30 aliquots of 100 ul of amplification product are applied to dots on a nitrocellulose filter set in a dot blot apparatus. The dots are then cut into separate dots and each dot is hybridized to a ³²P-labelled oligonucleotide specific for a single genotype of HCV. The
35 oligonucleotides to be used as hybridization probes are deduced from the consensus sequences shown in Figures 1A-1

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- ° thru 1H-5 or 6A-1 thru 6J-4 or from the SEQ ID NOs:
representing E1 or core sequences comprising genotypes 4a-
4f, 2c and 6a.

Example 8

5 ELISA Based on Synthetic Peptides Derived From E1 cDNA Sequences

E1 peptide(s) specific for genotype I/1a is
placed in 0.1% PBS buffer and 50ul of a 1mg/ml solution of
peptide is used to cover each well of the microtiter assay
10 plate. Serum samples from two mammals infected with
genotype I/1a HCV and from one mammal infected with
genotype 5a HCV are diluted as in Example 3 and the ELISA
is carried out as in Example 3. Both mammals infected with
genotype I HCV react positively with peptides while the
15 mammal infected with genotype 5a HCV exhibits no
reactivity. One skilled in the art would readily
understand that in the above experiment, core peptides
specific for genotype I/1a could be used in place of, or in
combination with the E1 genotype-specific peptide(s).

20 Example 9 Use of E1 Peptides as a Vaccine

Since the E1 genotype-specific peptides of the
present invention are derived from two variable regions in
the complete E1 protein, there exists support for the use
25 of these peptides as a vaccine to protect against a variety
of HCV genotypes. Mammals are immunized with peptide(s)
selected from SEQ ID NOs: 136-159 in an amount sufficient
to stimulate production of protective antibodies. The
immunized mammals challenged with various genotypes of HCV
30 are protected. One skilled in the art would readily
understand that genotype-specific core peptides of the
present invention could also be used either alone, in
combination with each other, or in combination with the
genotype-specific E1 peptides, as a vaccine to protect
35 against a variety of HCV genotypes. In addition, the above

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- ° vaccines may also be formulated using the universal core and/or E1 peptides of the present invention.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: BUKH, J., MILLER, R.H. AND
PURCELL, R.H.
- 5 (ii) TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
- 10 (iii) NUMBER OF SEQUENCES: 263
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
(B) STREET: 345 PARK AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
15 (F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WORDPERFECT 5.1
- 20 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE: 15-AUG-1995
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NO: 08/086,428
25 (B) FILING DATE: 29 JUNE 1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/290/665
(B) FILING DATE: 15 AUGUST 1994
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: RICHARD W. BORK
30 (B) REGISTRATION NUMBER: 36,459
(C) REFERENCE/DOCKET NUMBER: 2026-4116
- (viii) TELECOMMUNICATION INFORMATION:
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(B) TELEFAX: (212) 751-6849
(C) TELEX: 421792
- 35 (2) INFORMATION FOR SEQ ID NO:1:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK7

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	TAC	CAA	GTG	CGC	AAC	TCC	ACG	GGG	CTT	TAC	CAT	GTC	ACC	39
10	AAT	GAT	TGC	CCT	AAC	TCG	AGT	ATC	GTG	TAC	GAG	GCG	GCC	78
	GAT	GCC	ATC	CTG	CAC	ACT	CCG	GGG	TGT	GTC	CCT	TGC	GTT	117
	CGC	GAG	GGT	AAC	GTC	TCG	AGG	TGT	TGG	GTG	GCG	ATG	ACC	156
	CCC	ACG	GTG	GCC	ACC	AGG	GAT	GGC	AAA	CTC	CCC	ACA	GCG	195
	CAG	CTT	CGA	CGT	CAC	ATC	GAT	CTG	CTC	GTC	GGG	AGT	GCC	234
	ACC	CTC	TGT	TCG	GCC	CTC	TAC	GTG	GGG	GAC	CTG	TGC	GGG	273
	TCT	GTC	TTT	CTT	GTC	GGT	CAA	CTG	TTT	ACC	TTC	TCT	CCC	312
	AGG	CGC	CAC	TGG	ACG	ACG	CAA	GGC	TGC	AAT	TGT	TCT	ATC	351
15	TAT	CCT	GGC	CAT	ATA	ACG	GGT	CAC	CGC	ATG	GCG	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACC	ACG	GCG	TTG	GTA	GTA	429
	GCT	CAG	CTG	CTC	CGG	ATC	CCG	CAA	GCC	ATC	TTG	GAC	ATG	468
	ATC	GCT	GGT	GCT	CAC	TGG	GGA	GTC	CTG	GCG	GGC	ATA	GCG	507
	TAT	TTT	TCC	ATG	GTG	GGG	AAC	TGG	GCG	AAG	GTC	CTG	GTA	546
	GTG	CTG	CTG	CTA	TTT	GCC	GGC	GTC	GAC	GCG				576

20

- (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK9

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30	TAC	CAA	GTA	CGC	AAC	TCC	TCG	GGC	CTC	TAC	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCT	AAC	TCG	AGT	ATT	GTG	TAC	GAG	GCG	GCC	78
	GAT	GCC	ATC	CTG	CAT	TCT	CCA	GGG	TGT	GTC	CCT	TGC	GTT	117
	CGC	GAG	GGT	AAC	GCC	TCG	AAA	TGT	TGG	GTG	GCG	GTG	GCC	156
	CCC	ACG	GTG	GCC	ACC	AGG	GAC	GGC	AAG	CTC	CCC	GCA	ACG	195
	CAG	CTT	CGA	CGT	CAC	ATC	GAT	CTG	CTT	GTC	GGG	AGC	GCC	234
	ACC	CTC	TGC	TCG	GCC	CTC	TAT	GTG	GGG	GAC	TTG	TGC	GGG	273
	TCT	GTC	TTC	CTT	GTC	GGC	CAA	CTG	TTC	ACC	TTC	TCC	CCC	312
35	AGA	CGC	CAC	TGG	ACA	ACG	CAA	GAC	TGC	AAC	TGT	TCT	ATC	351

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TAC	CCC	GGC	CAT	ATT	ACG	GGT	CAT	CGC	ATG	GCG	TGG	GAT	390
ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACA	GCA	GCG	CTG	GTA	ATG	429
GCG	CAG	CTG	CTC	AGG	ATC	CCG	CAG	GCC	ATC	TTG	GAC	ATG	468
ATC	GCT	GGT	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	ATA	GCG	507
TAT	TTC	TCC	ATG	GTG	GGG	AAC	TGG	GCG	AAG	GTC	GTG	GTG	546
GTA	CTG	TTG	CTG	TTT	ACC	GGC	GTC	GAT	GCG				576

5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DR1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15	CAC	CAA	GTG	CGC	AAC	TCT	ACA	GGG	CTT	TAC	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCT	AAT	TCG	AGT	ATT	GTG	TAC	GAG	GCG	GCC	78
	GAT	GCC	ATC	CTG	CAC	GCG	CCG	GGG	TGT	GTC	CCT	TGC	GTT	117
	CGC	GAG	GGT	AAC	GCC	TCG	AGG	TGT	TGG	GTG	GCG	GTG	ACC	156
	CCC	ACG	GTG	GCC	ACC	AGG	GAC	GGC	AAA	CTC	CCC	ACA	ACG	195
	CAG	CTT	CGA	CGT	CAC	ATC	GAC	CTG	CTT	GTC	GGG	AGC	GCC	234
	ACC	CTC	TGC	TCG	GCC	CTC	TAC	GTG	GGG	GAC	CTG	TGC	GGG	273
20	TCT	GTC	TTC	CTT	GTC	GGT	CAA	CTG	TTC	ACC	TTT	TCT	CCC	312
	AGG	CGC	CAC	TGG	ACA	ACG	CAA	GAC	TGC	AAT	TGT	TCT	ATC	351
	TAT	CCC	GGC	CAT	ATA	ACG	GGA	CAC	CGT	ATG	GCA	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACG	ACA	GCG	CTG	GTA	ATG	429
	GCT	CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCC	ATC	TTG	GAC	ATG	468
	ATC	GCT	GGA	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	ATA	GCG	507
	TAT	TTC	TCC	ATG	GTG	GGG	AAC	TGG	GCG	AAG	GTC	GTG	GTA	546
25	GTG	CTG	TTG	CTG	TTT	GCC	GGC	GTT	GAT	GCG				576

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DR4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

35

- 85 -

CAC CAA GTG CGC AAC TCT ACA GGG CTT TAC CAT GTC ACC 39
 AAT GAT TGC CCT AAT TCG AGT ATT GTG TAC GAG GCG GCC 78
 GAT GCC ATC CTG CAC ACG CCG GGG TGT GTC CCT TGC GTT 117
 CGC GAG GGT AAC ACC TCG AGG TGT TGG GTG GCG GTG ACC 156
 CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC ACA ACG 195
 CAG CTC CGA CGT CAC ATC GAC CTG CTT GTC GGG AGC GCC 234
 5 ACC CTC TGC TCG GCC CTC TAC GTG GGG GAC TTG TGC GGG 273
 TCT GTC TTC CTT GTC GGT CAA CTG TTC ACC TTC TCT CCC 312
 AGG CAC CAC TGG ACA ACG CAA GAC TGC AAT TGT TCC ATC 351
 TAT CCC GGC CAT ATA ACG GGC CAC CGC ATG GCG TGG GAT 390
 ATG ATG ATG AAC TGG TCC CCT ACG ACA GCG CTG GTA GTA 429
 GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAC ATG 468
 ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG 507
 TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG GTA 546
 10 GTG CTG TTG CTG TTT GCC GGC GTT GAT GCG 576

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S14

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TAC CAA GTG CGC AAC TCC ACG GGG CTT TAC CAT GTT ACC 39
 AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG ACA GCT 78
 GAT GCT ATC CTA CAC GCT CCG GGA TGT GTC CCT TGC GTT 117
 CGT GAG GGT AAC ACC TCG AGG TGT TGG GTG GCG ATG ACC 156
 CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC GCA ACG 195
 25 CAG CTT CGA CGT TAC ATC GAT CTG CTT GTC GGG AGC GCC 234
 ACC CTC TGT TCG GCC CTC TAC GTG GGG GAC TTG TGC GGG 273
 TCT GTC TTT CTT GTC GGT CAG CTG TTT ACC TTC TCT CCC 312
 AGG CGC CTC TGG ACG ACG CAA GAC TGC AAT TGT TCT ATC 351
 TAT CCC GGC CAT ATA ACG GGT CAT CGC ATG GCA TGG GAT 390
 ATG ATG ATG AAC TGG TCC CCT ACG ACG GCA CTG GTA GTA 429
 GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAT ATG 468
 ATC GCT GGT GCT CAC TGG GGA GTC CTA GCG GGC ATA GCG 507
 30 TAT TTC TCC ATG GTG GGA AAC TGG GCG AAG GTC CTA GTG 546
 GTG CTG CTG CTA TTC GCC GGC GTT GAC GCG 576

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S18

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

	TAC	CAA	GTA	CGC	AAC	TCC	ACG	GGC	CTT	TAC	CAT	GTC	ACC	39
	AAT	GAC	TGC	CCT	AAC	TCG	AGC	ATT	GTG	TAC	GAG	ACG	GCC	78
	GAT	ACC	ATC	CTA	CAC	TCT	CCG	GGG	TGT	GTC	CCT	TGC	GTT	117
	CGC	GAG	GGT	AAC	GCC	TCG	AGA	TGT	TGG	GTG	CCG	GTG	GCC	156
	CCC	ACA	GTT	GCC	ACC	AGG	GAC	GGC	AAA	CTC	CCC	GCA	ACG	195
10	CAG	CTT	CGA	CGT	CAC	ATC	GAT	CTG	CTT	GTT	GGG	AGC	GCC	234
	ACC	CTC	TGC	TCG	GCC	CTC	TAT	GTG	GGG	GAC	CTG	TGC	GGG	273
	TCT	GTC	TTT	CTT	GTC	AGC	CAG	CTG	TTC	ACT	ATC	TCC	CCC	312
	AGG	CGC	CAC	TGG	ACA	ACG	CAA	GAC	TGC	AAC	TGT	TCT	ATC	351
	TAC	CCC	GGC	CAT	ATA	ACG	GGT	CAC	CGT	ATG	GCA	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACA	ACG	GCG	TTG	GTA	ATA	429
	GCT	CAG	CTG	CTC	AGG	GTC	CCG	CAA	GCC	GTC	TTG	GAC	ATG	468
15	ATC	GCT	GGT	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	ATA	GCG	507
	TAT	TTC	TCC	ATG	GCG	GGG	AAC	TGG	GCG	AAG	GTC	CTG	CTA	546
	GTG	CTG	TTG	CTG	TTT	GCC	GGC	GTC	GAT	GCG				576

(2) INFORMATION FOR SEQ ID NO:7:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
25 (C) INDIVIDUAL ISOLATE: SW1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	TAC	CAA	GTA	CGC	AAC	TCC	TCG	GGC	CTT	TAC	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCT	AAC	TCG	AGT	ATT	GTG	TAC	GAG	ACG	GCC	78
	GAT	GCC	ATT	CTA	CAC	TCT	CCA	GGG	TGT	GTC	CCT	TGC	GTT	117
	CGC	GAG	GAT	GGC	GCC	CCG	AAG	TGT	TGG	GTG	GCG	GTG	GCC	156
30	CCC	ACA	GTC	GCC	ACT	AGG	GAC	GGC	AAA	CTC	CCT	GCA	ACG	195
	CAG	CTT	CGA	CGT	CAC	ATC	GAT	CTG	CTT	GTC	GGA	AGC	GCC	234
	ACC	CTC	TGC	TCG	GCC	CTC	TAC	GTG	GGG	GAC	TTG	TGC	GGG	273
	TCT	GTC	TTT	CTC	GTC	AGT	CAA	CTG	TTC	ACG	TTC	TCC	CCC	312
	AGG	CGC	CAC	TGG	ACA	ACG	CAA	GAC	TGT	AAC	TGT	TCT	ATC	351
	TAT	CCC	GGC	CAC	ATA	ACG	GGT	CAC	GCG	ATG	GCA	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCC	CCC	ACA	ACA	GCG	CTG	GTA	GTA	429
35	GCT	CAG	CTG	CTC	AGG	ATC	CCG	CAA	GCC	GTC	TTG	GAC	ATG	468
	ATC	GCT	GGT	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	ATA	GCG	507

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TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG ATA 546
 GTG CTG TTG CTG TTT TCC GGC GTC GAT GCG 576

(2) INFORMATION FOR SEQ ID NO:8:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 10 (C) INDIVIDUAL ISOLATE: US11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAC CAA GTA CGC AAC TCC ACG GGG CTT TAC CAT GTC ACC 39
 AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG GCG GCC 78
 GAT GCC ATC CTG CAC ACT CCG GGG TGT GTT CCT TGC GTT 117
 15 CGC GAG GGT AAC GCT TCG AGG TGT TGG GTG GCG ATG ACC 156
 CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC ACA ACG 195
 CAA CTT CGA CGT CAC ATC GAT CTG CTT GTC GGG AGC GCC 234
 ACC CTC TGT TCG GCC CTC TAC GTG GGG GAC CTG TGC GGG 273
 TCT GTC TTT CTT GTC GGT CAA CTG TTT ACC TTC TCT CCC 312
 AGA CGC CAC TGG ACG ACG CAG GGC TGC AAT TGT TCT ATC 351
 TAT CCC GGC CAT ATA ACG GGT CAC CGC ATG GCA TGG GAT 390
 ATG ATG ATG AAC TGG TCC CCT ACG GCG GCG TTG GTG GTA 429
 20 GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAC ATG 468
 ATC GCT GGT GCT CAC TGG GGA GTC CTA GCG GGC ATA GCG 507
 TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG GTA 546
 GTG CTG CTG CTA TTT GCC GGC GTC GAC GCG 576

(2) INFORMATION FOR SEQ ID NO:9:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 30 (C) INDIVIDUAL ISOLATE: D1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TAT GAA GTG CGC AAC GTG TCC GGG GTG TAC CAT GTC ACG 39
 AAC GAC TGT TCC AAC TCG AGC ATT GTG TAT GAG ACA GCG 78
 GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT 117
 35 CGG GAG GAC AAC TCC TCT CGC TGC TGG GTA GCG CTC ACC 156
 CCC ACG CTC GCG GCT AGG AAT GGC AAC GTC CCC ACT ACG 195

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GCG ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT 234
 GCT TTC TGC TCC GCC ATG TAC GTG GGG GAT CTC TGC GGA 273
 TCT GTT TTC CTC ATC TCC CAG CTG TTC ACC CTC TCG CCT 312
 CGC CGG CAT GAG ACG GTA CAG GAG TGT AAT TGC TCA ATC 351
 TAT CCC GGC CAC GTG ACA GGT CAC CGT ATG GCT TGG GAT 390
 ATG ATG ATG AAC TGG TCA CCT ACA ACA GCC TTA GTG GTA 429
 5 TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC ATG GAC ATG 468
 GTG GCG GGG GCC CAC TGG GGG GTC CTG GCG GGC CTC GCC 507
 TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT 546
 GTG ATG CTA CTC TTT GCT GGC GTT GAC GGC 576

(2) INFORMATION FOR SEQ ID NO:10:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 15 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: D3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TAT GAA GTG CGC AAC GTG TCC GGG GTG TAC CAA GTC ACC 39
 AAT GAC TGT TCC AAC TCG AGC ATC GTG TAT GAG ACA GCG 78
 GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT 117
 20 CGG GAG GAC AAC TCC TCT CGC TGC TGG GTA GCG CTC ACC 156
 CCC ACG CTC GCG GCT AGG AAT AGC AGC GTC CCC ACT ACG 195
 ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT 234
 GCT TTC TGC TCC GCC ATG TAC GTG GGG GAT CTT TGC GGA 273
 TCT GTT TTC CTC GTC TCC CAG CTG TTC ACC TTC TCG CCT 312
 CGC CGG CAT GAG ACA GTA CAG GAA TGT AAC TGC TCA ATC 351
 TAT CCC GGC CAC GTG ACA GGT CAC CGC ATG GCT TGG GAT 390
 ATG ATG ATG AAC TGG TCG CCT ACA GCA GCC CTA GTG GTA 429
 25 TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG 468
 GTG GCG GGG GCC CAC TGG GGG GTC CTG GCG GGC CTC GCC 507
 TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT 546
 GTG ATG CTA CTC TTT GCT GGC GTC GAC GGC 576

(2) INFORMATION FOR SEQ ID NO:11:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 35 (A) ORGANISM: homosapiens

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(C) INDIVIDUAL ISOLATE: DK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	CAC	GTC	ACA	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATC	GTG	TAT	GAG	GCA	GTG	78
5	GAC	GTG	ATC	ATG	CAT	ACC	CCA	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	AAC	AAC	CAC	TCC	CGT	TGC	TGG	GTA	GCG	CTC	ACC	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	GCC	AGC	ATC	CCC	ACT	ACG	195
	ACA	ATA	CGA	CGC	CAT	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTT	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAC	CTC	TGC	GGA	273
	TCC	GTT	TTT	CTC	GTC	TCT	CAG	CTG	TTT	ACC	TTT	TCA	CCT	312
	CGC	CGG	CAT	GAG	ACA	GCA	CAG	GAC	TGC	AAC	TGC	TCA	ATC	351
10	TAT	CCC	GGC	CAC	GTT	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	ACA	GCC	CTA	GTG	CTA	429
	TCG	CAG	TTA	CTC	CGA	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	507
	TAC	TAC	TCC	ATG	GCG	GGG	AAC	TGG	GCC	AAG	GTT	TTA	ATT	546
	GTG	TTG	CTA	CTC	TTT	GCC	GGC	GTT	GAT	GGG				576

15 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATA	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	GTC	GTG	TAT	GAG	ACA	GCA	78
25	GAC	ATG	ATC	ATG	CAT	ACC	CCT	GGA	TGC	GTG	CCC	TGC	GTA	117
	CGG	GAG	AAC	AAC	TCC	TCC	CGC	TGT	TGG	GTA	GCG	CTC	ACT	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	GTC	AGC	GTC	CCC	ACC	ACG	195
	ACA	ATA	CGA	CGT	CAC	GTC	GAC	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCC	TTT	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
	TCT	GTT	TTT	CTT	GTC	TCC	CAG	CTG	TTT	ACC	TTT	TCG	CCT	312
	CGC	CGA	CAC	GAG	ACA	GTA	CAG	GAC	TGC	AAC	TGC	TCA	CTC	351
30	TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACA	GCA	GCC	CTA	GTG	GTG	429
	TCG	CAA	TTA	CTC	CGG	ATC	CCG	CAA	GCT	GTC	GTG	GAC	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GTG	GGA	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
	GTG	ATG	CTA	CTT	TTT	GCC	GGC	GTT	GAT	GGG				576

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° (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10	CAT GAA GTG CAC AAC GTA TCC GGG ATC TAC CAT GTC ACG	39
	AAC GAC TGC TCC AAC TCA AGT ATT GTG TAT GAG GCA GCG	78
	GAC ATG ATC ATG CAT ACC CCC GGG TGC GTG CCC TGC GTC	117
	CGG GAG AAC AAC TCC TCC CGT TGC TGG GTA GCG CTC ACT	156
	CCC ACG CTC GCG GCC AGG AAC GCC AGC ATC CCC ACT ACG	195
	ACA ATA CGA CGC CAT GTC GAC TTG CTC GTT GGG GCG GCT	234
	GCT TTC TGC TCC GCC ATG TAC GTG GGA GAT CTC TGC GGA	273
	TCT GTC TTC CTC GTC TCC CAG TTG TTC ACC TTC TCG CCT	312
15	CGC CGG CAT GAG ACG GTA CAG GAC TGC AAT TGC TCA ATC	351
	TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAT	390
	ATG ATG ATG AAC TGG TCA CCT ACA GCA GCC CTA GTG GTA	429
	TCG CAG TTA CTC CGA CTC CCA CAA GCT GTC ATG GAC ATG	468
	GTG GCG GGA GCC CAC TGG GGA GTC CTA GCG GGC CTT GCT	507
	TAC TAT TCC ATG GTG GGG AAC TGG GCC AAG GTT TTG ATT	546
	GTG ATG CTA CTC TTT GCC GGC GTT GAC GGG	576

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

30	TAT GAA GTG CGC AAC GTG TCC GGG GTA TAC CAT GTC ACG	39
	AAC GAC TGC TCC AAC TTA AGC ATC GTG TAC GAG ACA ACG	78
	GAC ATG ATC ATG CAC ACC CCT GGG TGC GTG CCC TGC GTT	117
	CGG GAA AAC AAC TCC TCC CGT TGT TGG GTA GCG CTC GCC	156
	CCC ACG CTC GCG GCC AGG AAC GCC AGC GTC CCC ACC ACG	195
	GCA ATA CGA CGC CAC GTC GAC TTG CTC GTT GGG GCG GCT	234
	GCT TTC TGC TCC GCT ATG TAC GTG GGG GAT CTT TGC GGA	273
	TCT GTT TTC CTC GTC TCC CAG CTG TTC ACC TTC TCG CCT	312
35	CGC CGA CAC GAG ACG GTA CAG GAC TGC AAC TGC TCA ATC	351

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TAT	CCC	GGC	CAC	GTA	ACA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	ACA	GCC	CTA	GTG	GTG	429
TCG	CAG	TTA	CTC	CGG	ATC	CCG	CAA	GCT	GTC	GTG	GAC	ATG	468
GTA	GCG	GGG	GCC	CAC	TGG	GGG	GTC	CTG	GCG	GGC	CTT	GCC	507
TAC	TAT	TCC	ATG	GTG	GGA	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
GTG	ATG	CTA	CTT	TTT	GCC	GGC	GTT	GAT	GGG				576

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

15	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATA	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATC	GTG	TAT	GAA	ACA	GCG	78
	GAC	ATG	ATT	ATG	CAT	ACC	CCT	GGA	TGC	ATG	CCC	TGC	GTT	117
	CGG	GAG	AAC	AAC	TCC	TCC	CGT	TGC	TGG	GTG	GCG	CTC	ACT	156
	CCC	ACG	CTC	GCG	GCT	AGG	AAT	GTC	AGC	GTC	CCC	ACT	ACG	195
	ACA	ATA	CGA	CGC	CAC	GTC	GAC	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
20	TCT	GTT	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	TTT	TCG	CCT	312
	CGC	CGA	CAC	GAG	ACG	GTA	CAG	GAC	TGC	AAC	TGC	TCA	ATC	351
	TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACA	ACA	GCC	CTA	GTG	GTG	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCG	CAA	GCT	ATC	GTG	GAC	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GTG	GGC	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
25	GTG	ATG	CTA	CTG	TTT	GCC	GGC	GTT	GAT	GGG				576

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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TAT GAA GTG CGC AAC GTG TCC GGG GTG TAC CAT GTC ACG 39
 AAC GAC TGC TCC AAC TCA AGT ATT GTG TAT GAG GCA GCG 78
 GAC ATG ATC ATG CAC ACT CCC GGG TGC GTG CCC TGC GTT 117
 CGG GAG GGC AAC TCC TCT CGC TGC TGG GTA GCG CTC ACT 156
 CCC ACT CTC GCG GCC AGG AAC GCC AGC GTC TCC ACC ACG 195
 ACA ATA CGA CAC CAC GTC GAT TTG CTC GTT GGG GCG GCT 234
 5 GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTA TGC GGA 273
 TCT GTT TTC CTC GTC TCC CAG CTG TTC ACC TTC TCA CCG 312
 CGC CGG CAT GAG ACA GTA CAG GAC TGC AAT TGC TCC ATC 351
 TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCC TGG GAT 390
 ATG ATG ATG AAC TGG TCA CCT ACA GCA GCC CTA GTG GTA 429
 TCG CAG TTG CTC CGG ATC CCA CAA GCT GTC GTG GAT ATG 468
 GTG GCG GGG GCC CAC TGG GGA ATC CTG GCG GGC CTT GCC 507
 TAC TAT TCC ATG GTA GGG AAC TGG GCT AAG GTT TTG ATT 546
 10 GTG ATG CTA CTC TTT GCC GGC GTT GAC GGG 576

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND8

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TAT GAG GTG CGC AAC GTG TCC GGG GTG TAC CAT GTC ACG 39
 AAC GAC TGC TCC AAC TCA AGT ATT GTG TAT GAG GCA GCG 78
 GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT 117
 CGG GAG GGC AAC TTC TCT AGT TGC TGG GTA GCG CTC ACT 156
 CCC ACT CTC GCG GCT AGG AAC GCC AGC GTC CCC ACC ACG 195
 25 ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT 234
 GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA 273
 TCT GTT TTC CTT GTC TCC CAG CTG TTC ACC TTC TCA CCG 312
 CGC CGG CAT GAG ACA GTA CAG GAC TGC AAT TGC TCC ATC 351
 TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAT 390
 ATG ATG ATG AAC TGG TCA CCT ACA GCG GCC CTA GTG GTA 429
 TCG CAG TTG CTC CGG ATC CCA CAA GCT GTC GTG GAT ATG 468
 GTG GCG GGG GCC CAC TGG GGA ATC CTG GCG GGC CTT GCC 507
 30 TAC TAT TCC ATG GTA GGG AAC TGG GCT AAG GTT TTG ATT 546
 GTG ATG CTA CTC TTT GCC GGC GTT GAC GGG 576

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 35 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: P10

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGT	ATT	GTG	TAT	GAG	GCA	GCG	78
	GAC	ATG	ATA	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGT	GTT	117
	CGG	GAG	AAC	AAC	TCC	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACT	156
	CCC	ACA	CTC	GCG	GCT	AGG	AAT	TCC	AGC	GTC	CCA	ACT	ACG	195
10	GCA	ATA	CGA	CGC	CAT	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
	TCT	GTT	CTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	TTC	TCA	CCT	312
	CGC	CGG	CAT	TGG	ACA	GTA	CAG	GAC	TGC	AAT	TGT	TCA	ATC	351
	TAT	CCT	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACA	GCA	GCC	CTA	GTG	GTG	429
	TCG	CAG	CTA	CTC	CGG	ATC	CCA	CAA	GCT	ATC	TTG	GAT	GTG	468
15	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTC	TTG	ATT	546
	GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTT	GAC	GGA				576

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
25 (C) INDIVIDUAL ISOLATE: S9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

	TAT	GAA	GTG	CGC	AAC	GTA	TCC	GGG	GCG	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGT	ATT	GTG	TAC	GAG	GCA	GCG	78
	GAC	GTG	ATC	ATG	CAT	ACC	CCC	GGG	TGT	GTA	CCC	TGC	GTT	117
	CAG	GAG	GGT	AAC	TCC	TCC	CAA	TGC	TGG	GTG	GCG	CTC	ACC	156
30	CCC	ACG	CTC	GCG	GCC	AGG	AAC	GCT	ACC	GTC	CCC	ACC	ACG	195
	ACA	ATA	CGA	CGT	CAT	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GTT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAC	CTG	TGC	GGA	273
	TCT	GTT	TTC	CTC	ATC	TCC	CAG	CTG	TTC	ACC	ATC	TCG	CCC	312
	CGT	CGG	CAT	GAG	ACA	GTA	CAG	AAC	TGC	AAT	TGC	TCA	ATC	351
	TAT	CCC	GGA	CAC	GTG	ACA	GGT	CAT	CGC	ATG	GCC	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	ACA	GCC	CTA	GTG	GTA	429
	TCG	CAG	CTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	ATG	GAT	ATG	468
35	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	507

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TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT 546
 GTG ATG CTA CTT TTT GCT GGT GTT GAC GGG 576

(2) INFORMATION FOR SEQ ID NO:20:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 10 (C) INDIVIDUAL ISOLATE: S45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GCG	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	TAT	GAG	GCA	GTG	78
	GAC	GTG	ATC	CTG	CAC	ACC	CCT	GGG	TGC	GTG	CCC	TGC	GTT	117
15	CGG	GAG	AAC	AAC	TCC	TCC	CGT	TGC	TGG	GTG	GCG	CTC	ACT	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	TCC	AGC	GTC	CCC	ACT	ACG	195
	ACA	ATA	CGA	CGT	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTT	GTT	TCC	CAG	CTG	TTC	ACC	TTC	TCG	CCT	312
	CGT	CGG	CAT	GAG	ACA	GTA	CAG	GAC	TGC	AAC	TGT	TCA	ATC	351
	TAT	CCC	GGC	CAC	GTA	ACA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
20	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	GCA	GCC	TTA	GTG	GTA	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	CTG	ATT	546
	GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTT	GAC	GGG				576

(2) INFORMATION FOR SEQ ID NO:21:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 30 (C) INDIVIDUAL ISOLATE: SA10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATG	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	TAT	GAG	GCA	CGG	78
	GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
35	CGG	GAG	AAC	AAC	TCC	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACT	156

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CCC ACG CTC GCG GCC AGG AAC TCC AGC GTC CCC ACT ACG 195
 ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT 234
 GCT TTC TGC TCC GCC ATG TAC GTG GGG GAC CTC TGC GGA 273
 TCT GTT TTC CTT GTC TCC CAG CTG TTC ACC TTC TCG CCT 312
 CGC CGG TAT GAG ACA GTA CAG GAC TGC AAT TGC TCA ATC 351
 TAT CCC GGC CGC GTA ACA GGT CAC CGC ATG GCT TGG GAT 390
 5 ATG ATG ATG AAC TGG TCA CCT ACA ACA GCT CTA GTA GTA 429
 TCG CAG TTA CTC CGG ATC CCA CAA GCT ATC GTG GAC ATG 468
 GTG GCG GGG GCC CAC TGG GGA GTC CTA GCG GGC CTT GCC 507
 TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT 546
 GTT ATG CTA CTC TTT GCC GGC GTT GAC GGG 576

(2) INFORMATION FOR SEQ ID NO:22:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

15

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL ISOLATE: SW2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TAT GAA GTG CGC AAC GTG TCC GGG GTG TAT CAT GTC ACG 39
 AAC GAC TGT TCC AAC TCA AGC ATT GTG TAT GAG ACA GCG 78
 20 GAC ATG ATC ATG CAT ACC CCC GGG TGC GTG CCC TGC GTT 117
 CGG GAG GCC AAC TCC TCC CGC TGC TGG GTA GCG CTC ACT 156
 CCC ACG CTA GCA GCC AGG AAC ACC AGC GTC CCC ACT ACG 195
 ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT 234
 GCT TTC TGC TCC GTT ATG TAC GTG GGG GAT CTC TGC GGA 273
 TCT GTT TTC CTC GTC TCC CAG CTG TTC ACT TTT TCA CCT 312
 CGC CGG CAC GAG ACA GTA CAG GAC TGC AAC TGT TCC ATC 351
 TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAC 390
 25 ATG ATG ATG AAC TGG TCA CCT ACA GCA GCC CTG GTG GTA 429
 TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG 468
 GTA GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCA 507
 TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT 546
 GTG ATG CTA CTC TTT GCT GGC GTT GAC GGG 576

30

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

35

- (vi) ORIGINAL SOURCE:

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(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

	TAC	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	TAT	GTC	ACG	39
5	AAC	GAC	TGT	TCC	AAC	TCA	AGC	ATT	GTG	TAT	GAG	ACA	GCG	78
	GAC	ATG	ATC	ATG	CAC	ACC	CCT	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	AGC	AAT	TCC	TCC	CGC	TGC	TGG	GTA	GCG	CTT	ACT	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	GCC	AGC	GTC	CCC	ACT	AAG	195
	ACA	ATA	CGA	CGT	CAC	GTC	GAC	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACT	TTC	TCG	CCT	312
	CGC	CGG	CAT	GAG	ACA	GTA	CAG	GAC	TGC	AAC	TGC	TCA	ATC	351
10	TAT	CCC	GGC	CAC	GTA	ACA	GGT	CAC	CGT	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACA	ACG	GCA	CTA	GTG	GTG	429
	TCG	CAG	TTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAC	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
	GTG	CTG	CTA	CTC	TTT	GCC	GGC	GTT	GAT	GGG				576

15 (2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATG	TAC	CAT	GTC	ACG	39
25	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	TTT	GAG	GCA	GCG	78
	GAC	TTG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	GGC	AAC	TCC	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACT	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	ACC	AGC	GTC	CCC	ACT	ACG	195
	ACG	ATA	CGA	CGC	CAT	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCT	ATG	TAT	GTG	GGA	GAC	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTC	GTC	TCT	CAG	CTG	TTC	ACC	TTC	TCG	CCT	312
30	CGC	CGG	CAT	GAG	ACT	TTG	CAG	GAC	TGC	AAC	TGC	TCA	ATC	351
	TAT	CCC	GGC	CAT	CTG	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCT	ACA	ACA	GCT	CTA	GTG	GTG	429
	TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	GTC	ATG	GAC	ATG	468
	GTG	ACA	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTT	GCC	507
	TAC	TAT	TCC	ATG	GCG	GGG	AAC	TGG	GCT	AAG	GTT	TTA	ATT	546
	GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTT	GAT	GGG				576

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(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

10	TAT GAA GTG CGC AAC GTG TCC GGG ATG TAC CAT GTC ACG	39
	AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA GCG	78
	GAC ATG ATC ATG CAC ACT CCC GGG TGC GTG CCC TGT GTT	117
	CGG GAG AAC AAT TCC TCC CGC TGC TGG GTA GCG CTC ACT	156
	CCC ACG CTC GCG GCC AGG AAC GCT AGC GTC CCC ACT ACG	195
	ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT	234
	ACT TTC TGC TCC GCT ATG TAC GTG GGG GAC CTC TGC GGG	273
15	TCC GTT TTC CTC ATC TCC CAG CTG TTC ACC TTC TCG CCT	312
	CGT CAG CAT GAG ACA GTA CAG GAC TGC AAT TGT TCA ATC	351
	TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAT	390
	ATG ATG ATG AAT TGG TCA CCT ACA GCA GCC CTA GTG GTA	429
	TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC ATG GAC ATG	468
	GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC	507
	TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT CTG ATT	546
20	GTG TTG CTA CTC TTT GCC GGC GTT GAC GGG	576

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

30	GCC CAA GTG AGG AAC ACC AGC CGC GGT TAC ATG GTG ACT	39
	AAC GAC TGT TCC AAT GAG AGC ATC ACC TGG CAG CTC CAA	78
	GCC GCG GTT CTC CAC GTC CCC GGG TGT ATC CCG TGT GAG	117
	AGG CTG GGA AAT ACA TCC CGA TGC TGG ATA CCG GTC ACA	156
	CCA AAC GTG GCC GTG CGG CAG CCC GGC GCT CTT ACG CAG	195
	GGC TTG CGG ACG CAC ATC GAC ATG GTT GTG ATG TCC GCC	234
	ACG CTC TGC TCT GCC CTC TAC GTG GGG GAC CTC TGC GGC	273
35	GGG GTG ATG CTC GCA GCC CAG ATG TTC ATT GTC TCG CCG	312

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CGA CGC CAC TGG TTT GTG CAA GAA TGC AAT TGC TCC ATC 351
TAC CCC GGT ACC ATC ACT GGA CAC CGT ATG GCA TGG GAC 390
ATG ATG ATG AAC TGG TCG CCC ACA GCC ACC ATG ATC CTG 429
GCG TAC GCG ATG CGC GTT CCC GAG GTC ATC ATA GAC ATC 468
ATC GGC GGG GCT CAC TGG GGC GTC ATG TTT GGC TTG GCC 507
TAC TTC TCT ATG CAG GGA GCG TGG GCG AAG GTC ATT GTC 546
ATC CTC TTG CTG GCT GCT GGG GTG GAC GCG 576

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCA CAA GTG AAG AAC ACC ACT AAC AGC TAC ATG GTG ACC 39
AAC GAC TGT TCT AAT GAC AGC ATC ACT TGG CAG CTC CAG 78
GCC GCG GTC CTC CAC GTC CCC GGG TGT GTC CCG TGC GAG 117
AAA ACG GGA AAT ACA TCT CGG TGC TGG ATA CCG GTT TCA 156
CCA AAC GTG GCC GTG CGG CAG CCC GGC GCC CTC ACG CAG 195
GGC TTG CGG ACG CAC ATT GAC ATG GTT GTG ATG TCC GCC 234
ACG CTC TGC TCT GCT CTT TAC GTG GGG GAC CTC TGC GGC 273
GGG GTG ATG CTC GCA GCC CAG ATG TTC ATC GTC TCG CCG 312
CAA CAT CAC TGG TTT GTG CAA GAC TGC AAT TGC TCT ATC 351
TAC CCT GGC ACC ATC ACT GGA CAC CGT ATG GCA TGG GAT 390
ATG ATG ATG AAC TGG TCG CCC ACG GCC ACC ATG ATC CTG 429
GCG TAC GCG ATG CGC GTT CCC GAG GTC ATC TTA GAC ATC 468
GTT AGC GGG GCA CAC TGG GGC GTC ATG TTC GGC TTG GCC 507
TAC TTC TCT ATG CAG GGA GCG TGG GCG AAA GTC GTT GTC 546
ATC CTT CTG CTG GCC GCT GGG GTG GAC GCG 576

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

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	GCC	GAA	GTG	AAG	AAC	ACC	AGT	ACC	AGC	TAC	ATG	GTG	ACA	39
	AAT	GAC	TGT	TCC	AAC	GAC	AGC	ATC	ACC	TGG	CAA	CTC	CAG	78
	GCC	GCG	GTC	CTC	CAC	GTC	CCC	GGG	TGC	GTC	CCG	TGC	GAG	117
	AGA	GTT	GGA	AAC	GCG	TCG	CGG	TGC	TGG	ATA	CCG	GTC	TCG	156
	CCA	AAC	GTA	GCT	GTG	CAG	CGG	CCT	GGC	GCC	CTC	ACG	CAG	195
5	GGC	TTG	CGG	ACG	CAC	ATC	GAC	ATG	GTT	GTG	ATG	TCC	GCC	234
	ACG	CTC	TGC	TCC	GCT	CTC	TAC	GTG	GGG	GAT	CTC	TGC	GGC	273
	GGG	GTA	ATG	CTC	GCC	GCT	CAG	ATG	TTC	ATT	ATC	TCG	CCG	312
	CAG	CAC	CAC	TGG	TTT	GTG	CAG	GAA	TGC	AAC	TGC	TCC	ATT	351
	TAC	CCT	GGT	ACC	ATC	ACT	GGA	CAC	CGT	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACA	ACC	ACC	ATG	ATC	TTG	429
	GCG	TAC	GCG	ATG	CGC	GTT	CCC	GAG	GTC	ATC	ATA	GAC	ATC	468
10	ATC	AGC	GGA	GCT	CAC	TGG	GGC	GTC	ATG	TTC	GGC	CTA	GCC	507
	TAC	TTC	TCT	ATG	CAG	GGA	GCG	TGG	GCG	AAG	GTC	GTT	GTC	546
	ATC	CTG	TTG	CTC	ACC	GCT	GGC	GTG	GAC	GCG				576

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

	GTC	CAA	GTG	AAA	AAC	ACC	AGT	ACC	AGC	TAT	ATG	GTG	ACC	39
	AAT	GAC	TGC	TCC	AAC	GAC	AGC	ATC	ACT	TGG	CAA	CTT	GAG	78
	GCT	GCG	GTC	CTC	CAC	GTT	CCC	GGG	TGT	GTC	CCG	TGC	GAG	117
	AAA	GTG	GGA	AAT	ACA	TCT	CGG	TGC	TGG	ATA	CCG	GTC	TCA	156
25	CCA	AAT	GTG	GCC	GTG	CAG	CGG	CCT	GGC	GCC	CTC	ACG	CAG	195
	GGC	TTG	CGG	ACT	CAC	ATC	GAC	ATG	GTC	GTG	ATG	TCC	GCC	234
	ACG	CTC	TGC	TCC	GCT	CTT	TAC	GTG	GGG	GAC	TTC	TGC	GGT	273
	GGG	ATG	ATG	CTC	GCA	GCC	CAA	ATG	TTC	ATT	GTC	TCG	CCG	312
	GCG	CAC	CAC	TCG	TTT	GTG	CAG	GAA	TGC	AAC	TGC	TCC	ATC	351
	TAC	CCC	GGT	ACC	ATC	ACC	GGG	CAC	CGT	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACG	GCC	ACT	TTG	ATC	CTG	429
	GCG	TAC	GTG	ATG	CGC	GTT	CCC	GAG	GTC	ATC	ATA	GAC	ATC	468
30	ATT	AGC	GGG	GCG	CAT	TGG	GGC	GTC	TTG	TTC	GGC	TTA	GCC	507
	TAC	TTC	TCT	ATG	CAG	GGA	GCG	TGG	GCG	AAA	GTC	GTT	GTC	546
	ATC	CTT	CTG	CTA	GCC	GCT	GGG	GTG	GAC	GCG				576

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi)

ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK8

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO:30:

	GTG	GAA	GTC	AGG	AAC	ATC	AGT	TCC	AGC	TAC	TAC	GCC	ACC	39
	AAT	GAT	TGC	TCA	AAC	AAC	AGC	ATC	ACC	TGG	CAA	CTC	ACC	78
	GAC	GCA	GTT	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CCA	TGT	GAG	117
10	AAT	GAC	AAT	GGC	ACC	CTG	CGC	TGC	TGG	ATA	CAA	GTG	ACA	156
	CCT	AAT	GTG	GCT	GTG	AAA	CAC	CGC	GGC	GCA	CTT	ACT	CAT	195
	AAC	CTG	CGA	ACA	CAC	GTC	GAC	GTG	ATC	GTA	ATG	GCA	GCT	234
	ACG	GTC	TGC	TCG	GCC	TTG	TAT	GTG	GGA	GAC	GTA	TGC	GGG	273
	GCC	GTG	ATG	ATC	GTG	TCG	CAG	GCT	CTC	ATA	ATA	TCG	CCT	312
	GAA	CGC	CAC	AAC	TTT	ACC	CAG	GAG	TGC	AAC	TGT	TCC	ATC	351
	TAC	CAA	GGT	CAT	ATC	ACC	GGC	CAC	CGC	ATG	GCA	TGG	GAC	390
	ATG	ATG	CTA	AAC	TGG	TCA	CCA	ACT	CTT	ACC	ATG	ATC	CTC	429
15	GCC	TAT	GCC	GCT	CGT	GTT	CCT	GAG	CTA	GCC	CTC	CAG	GTT	468
	GTC	TTC	GGC	GGC	CAT	TGG	GGC	GTG	GTG	TTT	GGC	TTG	GCC	507
	TAT	TTC	TCC	ATG	CAG	GGA	GCG	TGG	GCC	AAA	GTC	ATT	GCC	546
	ATC	CTC	CTT	CTT	GTC	GCA	GGA	GTG	GAT	GCA				576

(2) INFORMATION FOR SEQ ID NO:31:

(i)

SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi)

ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK11

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO:31:

	GTG	GAA	GTC	AGG	AAC	ACC	AGT	TCT	AGT	TAC	TAC	GCC	ACC	39
	AAT	GAT	TGC	TCA	AAC	AAC	AGC	ATC	ACC	TGG	CAA	CTC	ACC	78
	AAC	GCA	GTT	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CCA	TGT	GAG	117
30	AAT	GAC	AAT	GGC	ACC	CTG	CAC	TGC	TGG	ATA	CAA	GTG	ACA	156
	CCT	AAT	GTG	GCT	GTG	AAA	CAC	CGC	GGC	GCA	CTC	ACT	CAC	195
	AAC	CTG	CGA	GCA	CAT	ATA	GAT	ATG	ATT	GTA	ATG	GCA	GCT	234
	ACG	GTC	TGC	TCG	GCC	TTG	TAT	GTG	GGA	GAC	GTG	TGC	GGG	273
	GCC	GTG	ATG	ATC	GTG	TCG	CAG	GCT	TTC	ATA	GTA	TCG	CCA	312
	GAA	CAC	CAC	CAC	TTT	ACC	CAA	GAG	TGC	AAC	TGT	TCC	ATC	351
	TAC	CAA	GGT	CAC	ATC	ACC	GGC	CAC	CGC	ATG	GCA	TGG	GAC	390
	ATG	ATG	CTT	AAC	TGG	TCA	CCA	ACT	CTC	ACC	ATG	ATC	CTC	429
35	GCC	TAT	GCC	GCC	CGT	GTT	CCT	GAG	CTA	GTC	CTT	GAA	GTC	468
	GTC	TTC	GGT	GGT	CAT	TGG	GGT	GTG	GTG	TTT	GGC	TTG	GCC	507

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TAT TTC TCC ATG CAG GGA GCG TGG GCC AAG GTC ATT GCC 546
 ATC CTC CTT CTT GTA GCA GGA GTG GAT GCA 576

(2) INFORMATION FOR SEQ ID NO:32:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 10 (C) INDIVIDUAL ISOLATE: SW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

	GTG	GAA	GTC	AGG	AAC	ATC	AGT	TCT	AGC	TAC	TAT	GCC	ACC	39
	AAT	GAT	TGC	TCA	AAC	AGC	AGC	ATC	ACC	TGG	CAA	CTC	ACC	78
	AAC	GCA	GTC	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CCG	TGT	GAG	117
	AAT	GAT	AAT	GGC	ACC	CTG	CAC	TGC	TGG	ATA	CAA	GTG	ACA	156
15	CCT	AAT	GTG	GCT	GTG	AAA	CAC	CGC	GGC	GCG	CTC	ACT	CAC	195
	AAC	CTG	CGA	GCA	CAC	GTC	GAT	ATG	ATC	GTA	ATG	GCA	GCT	234
	ACG	GTC	TGC	TCG	GCC	TTG	TAT	GTG	GGA	GAC	ATG	TGC	GGG	273
	GCC	GTG	ATG	ATC	GTG	TCG	CAG	GCT	TTC	ATA	ATA	TCG	CCA	312
	GAA	CGC	CAC	AAC	TTT	ACC	CAA	GAG	TGC	AAC	TGT	TCC	ATC	351
	TAC	CAA	GGT	CGT	ATC	ACC	GGC	CAC	CGC	ATG	GCG	TGG	GAC	390
	ATG	ATG	CTA	AAC	TGG	TCA	CCA	ACT	CTT	ACC	ATG	ATC	CTT	429
20	GCC	TAT	GCC	GCT	CGT	GTT	CCT	GAG	CTA	GTC	CTT	GAA	GTT	468
	GTC	TTC	GGC	GGC	CAT	TGG	GGC	GTG	GTG	TTT	GGC	TTG	GCC	507
	TAT	TTC	TCC	ATG	CAA	GGA	GCG	TGG	GCC	AAG	GTC	ATT	GCC	546
	ATC	CTC	CTG	CTT	GTC	GCA	GGA	GTG	GAT	GCA				576

(2) INFORMATION FOR SEQ ID NO:33:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 30 (C) INDIVIDUAL ISOLATE: T8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

	GTG	GAA	GTT	AGA	AAC	ACC	AGT	TTT	AGC	TAC	TAC	GCC	ACC	39
	AAT	GAT	TGC	TCG	AAC	AAC	AGC	ATC	ACC	TGG	CAG	CTC	ACC	78
	AAC	GCA	GTT	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CCA	TGT	GAG	117
35	AAT	GAC	AAT	GGC	ACC	TTG	CGC	TGC	TGG	ATA	CAA	GTA	ACA	156

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CCT AAT GTG GCT GTG AAA CAC CGT GGC GCA CTC ACT CAC 195
 AAC CTG CGA ACG CAT GTC GAC GTG ATC GTA ATG GCA GCT 234
 ACG GTC TGC TCG GCC TTG TAT GTG GGG GAC GTG TGC GGG 273
 GCC GTG ATG ATA GCG TCG CAG GCT TTC ATA ATA TCG CCA 312
 GAA CGC CAC AAC TTC ACC CAG GAG TGC AAC TGT TCC ATC 351
 TAC CAA GGT CAT ATC ACC GGC CAC CGC ATG GCA TGG GAC 390
 5 ATG ATG CTG AAC TGG TCA CCA ACT CTC ACC ATG ATC CTC 429
 GCC TAC GCT GCT CGT GTG CCT GAA CTA GTC CTT GAA GTT 468
 GTC TTC GGC GGC CAT TGG GGC GTG GTG TTT GGC TTG GCC 507
 TAT TTC TCC ATG CAA GGA GCG TGG GCC AAA GTC ATC GCC 546
 ATC CTC CTC CTT GTC GCA GGA GTG GAC GCA 576

(2) INFORMATION FOR SEQ ID NO:34:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

15

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL ISOLATE: S83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTG GAG GTC AAG GAC ACC GGC GAC TCC TAC ATG CCG ACC 39
 AAC GAT TGC TCC AAC TCT AGT ATC GTT TGG CAG CTT GAA 78
 20 GGA GCA GTG CTT CAT ACT CCT GGA TGC GTC CCT TGT GAG 117
 CGT ACC GCC AAC GTC TCT CGA TGT TGG GTG CCG GTT GCC 156
 CCC AAT CTC GCC ATA AGT CAA CCT GGC GCT CTC ACT AAG 195
 GGC CTG CGA GCA CAC ATC GAT ATC ATC GTG ATG TCT GCT 234
 ACG GTC TGT TCT GCC CTT TAT GTG GGG GAC GTG TGT GGC 273
 GCG CTG ATG CTG GCC GCT CAG GTC GTC GTC GTG TCG CCA 312
 CAA CAC CAT ACG TTT GTC CAG GAA TGC AAC TGT TCC ATA 351
 25 TAC CCG GGC CGC ATT ACG GGA CAC CGC ATG GCT TGG GAT 390
 ATG ATG ATG AAC TGG TCG CCC ACT ACC ACC ATG CTC CTG 429
 GCG TAC TTG GTG CGC ATC CCG GAA GTC ATC TTG GAT ATT 468
 GTT ACA GGA GGT CAT TGG GGT GTA ATG TTT GGC CTC GCT 507
 TAC TTC TCC ATG CAG GGA TCG TGG GCG AAG GTC ATC GTT 546
 ATC CTC CTG CTG ACT GCT GGG GTG GAG GCG 576

30

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

35

- (vi) ORIGINAL SOURCE:

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(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

	TTA	GAG	TGG	CGG	AAT	GTG	TCC	GGC	CTC	TAC	GTC	CTT	ACC	39
	AAC	GAC	TGT	TCC	AAT	AGC	AGT	ATC	GTG	TAT	GAG	GCC	GAT	78
5	GAC	GTC	ATT	CTG	CAC	ACA	CCT	GGC	TGT	GTA	CCT	TGT	GTT	117
	CAG	GAC	GGC	AAT	ACA	TCT	ACG	TGC	TGG	ACC	TCA	GTG	ACG	156
	CCT	ACA	GTG	GCA	GTC	AGG	TAC	GTC	GGA	GCA	ACC	ACC	GCT	195
	TCG	ATA	CGC	AGT	CAT	GTG	GAC	CTG	CTA	GTG	GGC	GCG	GCC	234
	ACG	ATG	TGC	TCT	GCG	CTC	TAC	GTG	GGT	GAT	GTG	TGT	GGG	273
	GCC	GTC	TTC	CTT	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	CCT	312
	CGT	CGC	CAT	CAA	ACA	GTC	CAG	ACC	TGT	AAC	TGC	TCG	CTG	351
10	TAC	CCA	GGC	CAT	CTT	TCA	GGA	CAT	CGA	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAT	TGG	TCC	CCC	GCT	GTG	GGT	ATG	GTG	GTA	429
	GCG	CAC	GTC	CTG	CGT	CTG	CCC	CAG	ACC	TTG	TTC	GAC	ATA	468
	ATA	GCT	GGG	GCC	CAT	TGG	GGC	ATC	ATG	GCG	GGC	CTA	GCC	507
	TAT	TAC	TCC	ATG	CAG	GGC	AAC	TGG	GCC	AAG	GTC	GCT	ATC	546
	ATC	ATG	GTT	ATG	TTT	TCA	GGA	GTC	GAT	GCC				576

15 (2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

	CTA	GAG	TGG	CGG	AAT	GTG	TCT	GGC	CTC	TAT	GTC	CTT	ACC	39
	AAC	GAC	TGT	CCC	AAT	AGC	AGT	ATT	GTG	TAT	GAG	GCC	GAT	78
25	GAC	GTC	ATT	CTG	CAC	ACA	CCT	GGC	TGT	GTA	CCT	TGT	GTT	117
	CAG	GAC	GGC	AAT	ACA	TCC	ACG	TGC	TGG	ACC	TCG	GTG	ACA	156
	CCT	ACA	GTG	GCA	GTC	AGG	TAC	GTC	GGA	GCA	ACC	ACC	GCC	195
	TCG	ATA	CGC	AGT	CAT	GTG	GAC	CTG	TTA	GTG	GGC	GCG	GCC	234
	ACG	ATG	TGC	TCT	GCG	CTC	TAC	GTG	GGC	GAT	ATG	TGT	GGG	273
	GCC	GTC	TTC	CTC	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	CCG	312
	CGT	CGC	CAT	CAA	ACG	GTC	CAG	ACC	TGT	AAC	TGC	TCG	CTG	351
30	TAC	CCA	GGC	CAC	CTT	TCA	GGA	CAT	CGA	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAT	TGG	TCC	CCC	GCC	GTG	GGT	ATG	GTG	GTG	429
	GCG	CAC	GTC	CTG	CGG	TTG	CCC	CAG	ACC	TTG	TTC	GAC	ATA	468
	ATA	GCC	GGG	GCC	CAT	TGG	GGC	ATC	TTG	GCA	GGC	CTA	GCC	507
	TAT	TAC	TCC	ATG	CAG	GGC	AAC	TGG	GCC	AAG	GTC	GCT	ATC	546
	ATC	ATG	GTT	ATG	TTT	TCA	GGG	GTC	GAT	GCC				576

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(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

10	CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC CTC ACC	39
	AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT	78
	GAC GTT ATT CTG CAC ACA CCT GGC TGT GTA CCT TGT GTT	117
	CAG GAC GGT AAT ACA TCC ACG TGC TGG ACC CCA GTG ACA	156
	CCT ACA GTG GCA GTC AGG TAT GTC GGA GCA ACC ACC GCT	195
	TCG ATA CGC AGT CAT GTG GAC CTA TTG GTG GGC GCG GCC	234
	ACT ATG TGC TCT GCG CTC TAC GTG GGT GAT ATG TGT GGG	273
15	GCC GTC TTT CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT	312
	CGT CGC CAT CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG	351
	TAC CCA GGC CAT CTT TCA GGA CAT CGC ATG GCT TGG GAT	390
	ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTG	429
	GCG CAC GTT CTG CGT TTG CCC CAG ACC GTG TTC GAC ATA	468
	ATA GCC GGG GCC CAT TGG GGC ATC TTG GCG GGC CTA GCC	507
	TAT TAC TCC ATG CAA GGC AAC TGG GCC AAG GTC GCT ATC	546
20	ATC ATG GTT ATG TTT TCA GGG GTC GAC GCC	576

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

30	CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC CTT ACC	39
	AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT	78
	GAC GTC ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT	117
	CAG GAC GGC AAT ACA TCC ATG TGC TGG ACC CCA GTG ACA	156
	CCT ACG GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCT	195
	TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG GGC GCG GCC	234
	ACG CTG TGC TCT GCG CTC TAT GTG GGT GAT ATG TGT GGG	273
35	GCC GTC TTT CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT	312

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CGT CGC CAT CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG 351
TAC CCA GGC CAT GTT TCA GGA CAT CGA ATG GCT TGG GAT 390
ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTG 429
GCG CAC ATC CTG CGA TTG CCC CAG ACC TTG TTT GAC ATA 468
CTG GCC GGG GCC CAT TGG GGC ATC TTG GCG GGC CTA GCC 507
TAT TAT TCT ATG CAG GGC AAC TGG GCC AAG GTC GCT ATT 546
5 GTC ATG ATT ATG TTT TCA GGG GTC GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT ATC CTT ACC 39
AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT 78
GAC GTC ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT 117
CAG GAC GGC AAT ACA TCC ACG TGC TGG ACC CCA GTG ACA 156
CCT ACG GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCT 195
TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG GGC GCG GCC 234
20 ACG CTG TGC TCT GCG CTC TAT GTG GGT GAT ATG TGT GGG 273
GCC GTC TTT CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT 312
CGT CGC CAT CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG 351
TAC CCA GGC CAT CTT TCA GGA CAT CGA ATG GCT TGG GAT 390
ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTG 429
GCG CAC ATC CTG CGA TTG CCC CAG ACC TTG TTT GAC ATA 468
CTG GCC GGG GCC CAT TGG GGC ATC TTG GCG GGC CTA GCC 507
TAT TAT TCT ATG CAG GGC AAC TGG GCC AAG GTC GCT ATC 546
25 ATC ATG ATT ATG TTT TCA GGG GTC GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

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	GAG	CAC	TAC	CGG	AAT	GCT	TCG	GGC	ATC	TAT	CAC	ATC	ACC	39
	AAT	GAT	TGT	CCG	AAT	TCC	AGT	ATA	GTC	TAT	GAA	GCT	GAC	78
	CAT	CAC	ATC	CTA	CAC	TTG	CCG	GGG	TGC	GTA	CCC	TGT	GTG	117
	ATG	ACT	GGG	AAC	ACA	TCG	CGT	TGC	TGG	ACG	CCG	GTG	ACG	156
	CCT	ACA	GTG	GCT	GTC	GCA	CAC	CCG	GGC	GCT	CCG	CTT	GAG	195
5	TCG	TTC	CGG	CGA	CAT	GTG	GAC	TTA	ATG	GTA	GGC	GCG	GCC	234
	ACT	TTG	TGT	TCT	GCC	CTC	TAT	GTT	GGG	GAC	CTC	TGC	GGA	273
	GGT	GCC	TTC	CTG	ATG	GGG	CAG	ATG	ATC	ACT	TTT	CGG	CCG	312
	CGT	CGC	CAC	TGG	ACC	ACG	CAG	GAG	TGC	AAT	TGT	TCC	ATC	351
	TAC	ACT	GGC	CAT	ATC	ACC	GGC	CAC	AGG	ATG	GCG	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	AGC	CCT	ACC	ACC	ACT	CTG	CTC	CTC	429
	GCC	CAG	ATC	ATG	AGG	GTC	CCC	ACA	GCC	TTT	CTC	GAC	ATG	468
10	GTT	GCC	GGA	GGC	CAC	TGG	GGC	GTC	CTC	GCG	GGC	TTG	GCG	507
	TAC	TTC	AGC	ATG	CAA	GGC	AAT	TGG	GCC	AAG	GTA	GTC	CTG	546
	GTC	CTT	TTC	CTC	TTT	GCT	GGG	GTA	GAC	GCC				576

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: Z1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

	GTG	CAC	TAC	CGG	AAT	GCT	TCG	GGC	GTC	TAT	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCT	AAC	ACC	AGC	ATA	GTG	TAC	GAG	ACG	GAG	78
	CAC	CAC	ATC	ATG	CAC	TTG	CCA	GGG	TGT	GTC	CCC	TGT	GTG	117
	CGG	ACG	GAG	AAT	ACT	TCT	CGC	TGC	TGG	GTG	CCC	TTG	ACC	156
25	CCC	ACT	GTG	GCC	GCG	CCC	TAT	CCC	AAC	GCA	CCG	TTA	GAG	195
	TCC	ATG	CGC	AGG	CAT	GTA	GAC	CTG	ATG	GTG	GGT	GCG	GCT	234
	ACT	ATG	TGT	TCC	GCC	TTC	TAC	ATT	GGA	GAT	CTG	TGT	GGA	273
	GGC	GTC	TTC	CTA	GTG	GGC	CAG	CTG	TTC	GAC	TTC	CGA	CCG	312
	CGC	CGG	CAC	TGG	ACC	ACC	CAG	GAT	TGC	AAC	TGC	TCC	ATC	351
	TAT	CCT	GGT	CAC	GTC	TCG	GGC	CAC	AGG	ATG	GCC	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	AGC	CCT	ACC	AGC	GCG	CTG	ATT	ATG	429
30	GCT	CAG	ATC	TTA	CGG	ATC	CCC	TCT	ATC	CTA	GGT	GAC	TTG	468
	CTC	ACC	GGG	GGT	CAC	TGG	GGA	GTT	CTT	GCT	GGT	CTA	GCT	507
	TTC	TTC	AGC	ATG	CAG	AGT	AAC	TGG	GCG	AAG	GTC	ATC	CTG	546
	GTC	CTA	TTC	CTC	TTT	GCC	GGG	GTC	GAG	GGA				576

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

	GTT	AAC	TAT	CGC	AAT	GCC	TCG	GGC	GTC	TAT	CAC	GTC	ACC	39
	AAC	GAC	TGC	CCG	AAC	TCG	AGC	ATA	GTG	TAT	GAG	GCC	GAA	78
	CAC	CAG	ATC	TTA	CAC	CTC	CCA	GGG	TGC	TTG	CCC	TGT	GTG	117
	AGG	GTT	GGG	AAT	CAG	TCA	CGC	TGC	TGG	GTG	GCC	CTT	ACT	156
10	CCC	ACC	GTG	GCG	GTG	TCT	TAT	ATC	GGT	GCT	CCG	CTT	GAC	195
	TCC	CTC	CGG	AGA	CAT	GTG	GAC	CTG	ATG	GTG	GGC	GCC	GCT	234
	ACT	GTA	TGC	TCT	GCC	CTC	TAC	GTT	GGA	GAT	CTG	TGC	GGT	273
	GGT	GCA	TTC	TTG	GTT	GGC	CAG	ATG	TTC	TCC	TTC	CAG	CCG	312
	CGA	CGC	CAC	TGG	ACT	ACG	CAG	GAC	TGC	AAT	TGT	TCT	ATC	351
	TAC	GCA	GGG	CAT	ATC	ACG	GGC	CAC	AGG	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	AGT	CCC	ACA	ACC	ACC	CTG	CTT	CTC	429
15	GCC	CAG	GTC	ATG	AGG	ATC	CCT	AGC	ACT	CTG	GTA	GAT	CTA	468
	CTC	GCT	GGA	GGG	CAC	TGG	GGC	GTC	CTT	GTT	GGG	TTG	GCG	507
	TAC	TTC	AGT	ATG	CAA	GCT	AAT	TGG	GCC	AAA	GTC	ATC	CTG	546
	GTC	CTT	TTC	CTC	TTC	GCT	GGA	GTT	GAT	GCC				576

(2) INFORMATION FOR SEQ ID NO:43:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

	GTC	AAC	TAT	CAC	AAT	GCC	TCG	GGC	GTC	TAT	CAC	ATC	ACC	39
	AAC	GAC	TGC	CCG	AAC	TCG	AGC	ATA	ATG	TAT	GAG	GCC	GAA	78
	CAC	CAC	ATC	CTA	CAC	CTC	CCA	GGG	TGC	GTA	CCC	TGT	GTG	117
	AGG	GAG	GGG	AAC	CAG	TCA	CGC	TGC	TGG	GTG	GCC	CTT	ACT	156
30	CCC	ACC	GTG	GCG	GCG	CCT	TAT	ATC	GGT	GCA	CCG	CTT	GAA	195
	TCC	ATC	CGG	AGA	CAT	GTG	GAC	CTG	ATG	GTA	GGC	GCT	GCT	234
	ACA	GTG	TGC	TCC	GCT	CTC	TAC	ATT	GGG	GAC	CTG	TGC	GGT	273
	GGC	GTA	TTT	TTG	GTT	GGT	CAG	ATG	TTT	TCT	TTC	CAG	CCG	312
	CGA	CGC	CAC	TGG	ACT	ACG	CAG	GAC	TGC	AAT	TGT	TCC	ATC	351
	TAT	GCG	GGG	CAC	GTT	ACA	GGC	CAC	AGA	ATG	GCA	TGG	GAC	390
35	ATG	ATG	ATG	AAC	TGG	AGT	CCC	ACA	ACC	ACC	TTG	GTC	CTC	429
	GCC	CAG	GTT	ATG	AGG	ATC	CCT	AGC	ACT	CTG	GTG	GAC	CTA	468

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CTC	ACT	GGA	GGG	CAC	TGG	GGT	ATC	CTT	ATC	GGG	GTG	GCA	507
TAC	TTC	TGC	ATG	CAA	GCT	AAT	TGG	GCC	AAG	GTC	ATT	CTG	546
GTC	CTT	TTC	CTC	TAC	GCT	GGA	GTT	GAT	GCC				576

(2) INFORMATION FOR SEQ ID NO:44:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK13

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TAC	AAC	TAT	CGC	AAC	AGC	TCG	GGT	GTC	TAC	CAT	GTC	ACC	39
AAC	GAT	TGC	CCG	AAC	TCG	AGC	ATA	GTC	TAT	GAA	ACC	GAT	78
TAC	CAC	ATC	TTA	CAC	CTC	CCG	GGA	TGC	GTT	CCT	TGC	GTG	117
AGG	GAA	GGG	AAC	AAG	TCT	ACA	TGC	TGG	GTG	TCT	CTC	ACC	156
CCC	ACC	GTG	GCT	GCG	CAA	CAT	CTG	AAT	GCT	CCG	CTT	GAG	195
TCT	TTG	AGA	CGT	CAC	GTG	GAT	CTG	ATG	GTG	GGC	GGC	GCC	234
ACT	CTC	TGC	TCC	GCC	CTC	TAC	ATC	GGA	GAC	GTG	TGT	GGG	273
GGT	GTG	TTC	TTG	GTC	GGT	CAA	CTG	TTC	ACC	TTC	CAA	CCT	312
CGC	CGC	CAC	TGG	ACC	ACC	CAA	GAC	TGC	AAT	TGT	TCC	ATC	351
TAC	ACA	GGA	CAT	ATC	ACA	GGA	CAC	AGA	ATG	GCT	TGG	GAC	390
ATG	ATG	ATG	AAT	TGG	AGC	CCC	ACT	GCG	ACG	CTG	GTC	CTC	429
GCC	CAA	CTT	ATG	AGG	ATC	CCA	GGC	GCC	ATG	GTC	GAC	CTG	468
CTT	GCA	GGC	CAC	TGG	GGC	ATT	CTG	GTT	GGC	ATA	GCG		507
TAC	TTC	AGC	ATG	CAA	GCT	AAT	TGG	GCC	AAG	GTT	ATC	CTG	546
GTC	CTG	TTT	CTC	TTT	GCT	GGA	GTC	GAC	GCT				576

25

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA1

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTT	CCC	TAC	CGG	AAT	GCC	TCT	GGG	GTT	TAC	CAT	GTC	ACC	39
AAT	GAC	TGC	CCA	AAC	TCC	TCC	ATA	GTC	TAC	GAG	GCT	GAT	78
AGC	CTG	ATC	TTG	CAC	GCA	CCT	GGC	TGC	GTG	CCC	TGT	GTC	117

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5
 AGG CAA GAT AAT GTC AGT AGG TGC TGG GTC CAA ATC ACC 156
 CCC ACA CTG TCA GCC CCG ACC TTC GGA GCG GTC ACG GCT 195
 CCT CTT CGG AGG GCC GTT GAC TAC TTA GCG GGA GGA GCT 234
 GCT CTC TGC TCC GCA CTA TAC GTC GGC GAC GCG TGC GGG 273
 GCA GTG TTT CTG GTA GGC CAA ATG TTC ACC TAT AGG CCT 312
 CGC CAG CAT ACC ACA GTG CAG GAC TGC AAC TGT TCC ATT 351
 TAC AGT GGC CAT ATC ACC GGC CAC CGG ATG GCT TGG GAC 390
 ATG ATG ATG AAT TGG TCA CCT ACG ACA GCC TTG CTG ATG 429
 GCC CAG ATG ATG CTA CGG ATC CCC CAG GTG GTC ATA GAC ATC 468
 ATA GCC GGG GGC CAC TGG GGG GTC TTG TTT GCC GCC GCA 507
 TAC TTT GCG TCG GCC GCC AAC TGG GCT AAG GTA GTG CTG 546
 GTT CTG TTC CTG TTT GCG GGG GTC GAT GGC 576

10 (2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

20 GTT CCC TAC CGA AAC GCC TCT GGG GTT TAT CAT GTC ACC 39
 AAT GAT TGC CCA AAC TCT TCC ATA GTT TAC GAG GCT GAT 78
 AAC CTG ATC TTG CAT GCA CCT GGT TGC GTG CCT TGT GTC 117
 AGG CAA GAT AAT GTC AGT AAG TGC TGG GTC CAA ATC ACC 156
 CCC ACG TTG TCA GCC CCG AAT CTC GGA GCG GTC ACG GCT 195
 CCT CTT CGG AGG GCC GTT GAC TAC TTA GCG GGA GGG GCT 234
 GCC CTC TGC TCC GCA CTA TAC GTC GGG GAC GCG TGC GGG 273
 GCA GTG TTT TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT 312
 CGC CAG CAC ACT ACG GTG CAA GAC TGC AAT TGC TCT ATT 351
 25 TAC AGT GGC CAT ATC ACC GGC CAC CGG ATG GCA TGG GAC 390
 ATG ATG ATG AAT TGG TCA CCT ACG ACG GCC TTG CTG ATG 429
 GCC CAG TTG CTA CGG ATT CCC CAG GTG GTC ATC GAC ATC 468
 ATT GCC GGG GGC CAC TGG GGG GTC TTG TTT GCC GCC GCA 507
 TAT TTC GCG TCA GCG GCT AAC TGG GCT AAG GTT ATA CTG 546
 GTC TTG TTT CTG TTT GCG GGG GTC GAT GCC 576

30 (2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

	GTC	CCC	TAC	CGA	AAT	GCC	TCT	GGG	GTT	TAT	CAT	GTC	ACC	39
5	AAT	GAT	TGC	CCA	AAC	TCT	TCC	ATA	GTC	TAC	GAG	GCT	GAT	78
	AAC	CTG	ATT	CTG	CAC	GCA	CCT	GGT	TGC	GTG	CCC	TGT	GTC	117
	AAG	GAA	GGT	AAT	GTC	AGT	AGG	TGC	TGG	GTC	CAA	ATC	ACC	156
	CCC	ACA	TTG	TCA	GCC	CCG	AAC	CTC	GGA	GCG	GTC	ACG	GCT	195
	CCT	CTT	CGG	AGG	GTC	GTT	GAC	TAC	TTA	GCG	GGA	GGG	GCT	234
	GCC	CTC	TGC	TCC	GCA	CTA	TAC	GTC	GGG	GAC	GCG	TGC	GGG	273
	GCA	GTG	TTC	TTG	GTA	GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	312
	CGC	CAG	CAT	ACT	ACG	GTG	CAG	GAC	TGC	AAC	TGT	TCC	ATT	351
10	TAC	AGC	GGC	CAT	ATC	ACC	GGC	CAC	CGA	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAT	TGG	TCA	CCT	ACG	ACA	GCC	TTG	GTG	ATG	429
	GCC	CAG	GTG	CTA	CGG	ATT	CCC	CAA	GTG	GTC	ATT	GAC	ATC	468
	ATT	GCC	GGG	GGC	CAC	TGG	GGG	GTC	TTG	TTC	GCC	GTC	GCA	507
	TAC	TTC	GCG	TCA	GCG	GCT	AAC	TGG	GCT	AAG	GTT	GTG	CTG	546
	GTC	CTG	TTT	CTG	TTT	GCG	GGG	GTC	GAT	GGC				576

15 (2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

	GTT	CCT	TAC	CGG	AAT	GCC	TCT	GGG	GTG	TAT	CAT	GTT	ACC	39
25	AAT	GAT	TGC	CCA	AAC	TCT	TCC	ATA	GTC	TAT	GAG	GCT	GAT	78
	GAC	CTG	ATC	CTA	CAC	GCA	CCT	GGC	TGC	GTG	CCC	TGT	GTC	117
	CGG	AAG	GAT	AAT	GTC	AGT	AGA	TGC	TGG	GTT	CAT	ATC	ACC	156
	CCC	ACA	CTA	TCA	GCC	CCG	AGC	CTC	GGA	GCG	GTC	ACG	GCT	195
	CCT	CTT	CGG	AGG	GCC	GTT	GAT	TAC	TTG	GCG	GGA	GGG	GCC	234
	GCC	CTG	TGC	TCC	GCG	TTA	TAC	GTC	GGA	GAC	GTG	TGC	GGG	273
	GCA	TTG	TTT	TTG	GTA	GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	312
30	CGC	CAG	CAT	GCT	ACG	GTA	CAG	GAC	TGC	AAC	TGC	TCC	ATT	351
	TAC	AGT	GGC	CAT	ATC	ACT	GGC	CAC	CGG	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAT	TGG	TCA	CCC	GCG	ACA	GCC	TTG	GTG	ATG	429
	GCC	CAA	ATG	CTA	CGG	ATT	CCC	CAG	GTG	GTC	ATT	GAC	ATC	468
	ATT	GCC	GGG	GGC	CAC	TGG	GGG	GTC	TTG	TTC	GCC	GCT	GCA	507
	TAC	TTC	GCG	TCG	GCG	GCT	AAC	TGG	GCT	AAG	GTT	GTG	CTG	546
	GTC	TTG	TTT	CTG	TTT	GCG	GGG	GTT	GAT	GCC				576

35

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(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

10	GTC CCC TAC CGA AAT GCC TCC GGG GTT TAT CAT GTC ACC	39
	AAT GAT TGC CCG AAC TCT TCC ATA GTC TAT GAG GCT GAC	78
	AAC CTG ATC CTG CAC GCA CCT GGT TGC GTG CCC TGT GTC	117
	AGA CAA AAT AAT GTC AGT AGG TGC TGG GTC CAA ATC ACC	156
	CCC ACA TTG TCA GCC CCG AAC CTC GGA GCG GTC ACG GCT	195
	CCT CTT CGG AGG GCC GTT GAC TAC CTA GCG GGA GGG GCT	234
	GCC CTC TGC TCC GCG CTA TAC GTC GGG GAC GCG TGC GGG	273
15	GCA GTG TTT TTG GTA GGC CAG ATG TTC AGC TAT AGG CCT	312
	CGC CAG CAC ACT ACG GTG CAG GAC TGC AAC TGT TCC ATT	351
	TAC AGT GGC CAT ATC ACC GGC CAC CGA ATG GCA TGG GAC	390
	ATG ATG ATG AAT TGG TCA CCT ACG ACA GCC TTG GTG ATG	429
	GCC CAG TTG CTA CGG ATT CCC CAG GTG GTC ATC GAC ATC	468
	ATT GCC GGG GGC CAC TGG GGG GTC TTG TTC GCC GCC GCA	507
	TAT TTC GCG TCA GCG GCT AAC TGG GCT AAG GTT GTG CTG	546
20	GTC TTG TTT CTG TTT GCG GGG GTC GAT GCC	576

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

30	GTT CCC TAC CGA AAT GCC TCT GGG GTT TAT CAT GTC ACC	39
	AAT GAT TGC CCA AAC TCT TCC ATC GTC TAC GAG GCT GAT	78
	GAC CTG ATC TTA CAC GCA CCT GGT TGC GTG CCC TGT GTT	117
	AGG CAG GGT AAT GTC AGT AGG TGC TGG GTC CAG ATC ACC	156
	CCC ACA CTG TCA GCC CCG AGC CTC GGA GCG GTC ACG GCT	195
	CCT CTT CGG AGG GCC GTT GAC TAC TTA GCG GGG GGG GCT	234
	GCC CTT TGC TCC GCG TTA TAC GTC GGA GAC GCG TGC GGG	273
35	GCA GTG TTT TTG GTA GGT CAA ATG TTC ACC TAT AGC CCT	312
	CGC CGG CAT AAT GTT GTG CAG GAC TGC AAC TGT TCC ATT	351

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TAC AGT GGC CAC ATC ACC GGC CAC CGG ATG GCA TGG GAC 390
 ATG ATG ATG AAT TGG TCA CCT ACA ACA GCT TTG GTG ATG 429
 GCC CAG TTG TTA CGG ATT CCC CAG GTG GTC ATT GAC ATC 468
 ATT GCC GGG GCC CAC TGG GGG GTC TTG TTC GCC GCC GCA 507
 TAC TAC GCG TCG GCG GCT AAC TGG GCC AAG GTT GTG CTG 546
 GTC CTG TTT CTG TTT GCG GGG GTC GAT GCC 576

5

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

15 CTT ACC TAC GGC AAC TCC AGT GGG CTA TAC CAT CTC ACA 39
 AAT GAT TGC CCC AAC TCC AGC ATC GTG CTG GAG GCG GAT 78
 GCT ATG ATC TTG CAT TTG CCT GGA TGC TTG CCT TGT GTG 117
 AGG GTC GAT GAT CGG TCC ACC TGT TGG CAT GCT GTG ACC 156
 CCC ACC CTG GCC ATA CCA AAT GCT TCC ACG CCC GCA ACG 195
 GGA TTC CGC AGG CAT GTG GAT CTT CTT GCG GGC GCC GCA 234
 GTG GTT TGC TCA TCC CTG TAC ATC GGG GAC CTG TGT GGC 273
 20 TCT CTC TTT TTG GCG GGA CAA CTA TTC ACC TTT CAG CCC 312
 CGC CGT CAT TGG ACT GTG CAA GAC TGC AAC TGC TCC ATC 351
 TAT ACA GGC CAC GTC ACC GGC CAC AGG ATG GCT TGG GAC 390
 ATG ATG ATG AAC TGG TCA CCC ACA ACC ACT CTG GTC CTA 429
 TCT AGC ATC TTG AGG GTA CCT GAG ATT TGT GCG AGT GTG 468
 ATA TTT GGT GGC CAT TGG GGG ATA CTA CTA GCC GTT GCC 507
 TAC TTT GGC ATG GCT GGC AAC TGG CTA AAA GTT CTG GCT 546
 25 GTT CTG TTC CTA TTT GCA GGG GTT GAA GCA 576

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

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	Tyr	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	Leu
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Val	Ser
					35					40					45
5	Arg	Cys	Trp	Val	Ala	Met	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly
					50					55					60
	Lys	Leu	Pro	Thr	Ala	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
10	Arg	His	Trp	Thr	Thr	Gln	Gly	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ala	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Ile	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
15	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
	Leu	Val	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Ala			
					185					190					

(2) INFORMATION FOR SEO ID NO:53:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

25

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

30	Tyr	Gln	Val	Arg	Asn	Ser	Ser	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	Leu
					20					25					30
	His	Ser	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ala	Ser
					35					40					45
	Lys	Cys	Trp	Val	Ala	Val	Ala	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly
					50					55					60
35	Lys	Leu	Pro	Ala	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val
					65					70					75

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Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 5 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 10 Val Val Val Leu Leu Leu Phe Thr Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DR1

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

His Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
 5 10 15
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu
 20 25 30
 25 His Ala Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
 35 40 45
 Arg Cys Trp Val Ala Val Thr Pro Thr Val Ala Thr Arg Asp Gly
 50 55 60
 Lys Leu Pro Thr Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
 65 70 75
 Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
 80 85 90
 30 Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro
 140 145 150
 35

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°	Gln	Ala	Ile	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
	Val	Val	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Ala			
					185					190					

5 (2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DR4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

15	His	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	Leu
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Thr	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Val	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly
					50					55					60
20	Lys	Leu	Pro	Thr	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
	His	His	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
25	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ala	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Ile	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
30	Leu	Val	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Ala			
					185					190					

(2) INFORMATION FOR SEO ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids

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(B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

	Tyr	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp	
					5					10						15
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Ala	Ile	Leu	
					20					25						30
10	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Thr	Ser	
					35					40						45
	Arg	Cys	Trp	Val	Ala	Met	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly	
					50					55						60
	Lys	Leu	Pro	Ala	Thr	Gln	Leu	Arg	Arg	Tyr	Ile	Asp	Leu	Leu	Val	
					65					70						75
	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85						90
15	Gly	Ser	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	
					95					100						105
	Arg	Leu	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115						120
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130						135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ala	Gln	Leu	Leu	Arg	Ile	Pro	
20					140					145						150
	Gln	Ala	Ile	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160						165
	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	
					170					175						180
	Leu	Val	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Ala				
					185					190						

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

0	Tyr	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Thr	Ile	Leu
					20					25					30
	His	Ser	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ala	Ser
					35					40					45
	Arg	Cys	Trp	Val	Pro	Val	Ala	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly
					50					55					60
5	Lys	Leu	Pro	Ala	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg
					95					100					105
	Arg	His	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
10	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Ile	Ala	Gln	Leu	Leu	Arg	Val	Pro
					140					145					150
	Gln	Ala	Val	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Ala	Gly	Asn	Trp	Ala	Lys	Val
15					170					175					180
	Leu	Leu	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Ala			
					185					190					

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

25 (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SW1

	Tyr	Gln	Val	Arg	Asn	Ser	Ser	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
30	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Ala	Ile	Leu
					20					25					30
	His	Ser	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asp	Gly	Ala	Pro
					35					40					45
	Lys	Cys	Trp	Val	Ala	Val	Ala	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly
					50					55					60
	Lys	Leu	Pro	Ala	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val
					65					70					75
35	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90

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Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 5 Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Leu Leu Leu Phe Ser Gly Val Asp Ala
 185 190

10

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

20

Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
 5 10 15
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
 35 40 45
 25 Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly
 50 55 60
 Lys Leu Pro Thr Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
 65 70 75
 Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 30 Arg His Trp Thr Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 35

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° Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:60:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: D1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asp Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Gly
 50 55 60
 Asn Val Pro Thr Thr Ala Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Ile Ser Gln Leu Phe Thr Leu Ser Pro Arg
 95 100 105
 Arg His Glu Thr Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

30

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown

35

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(D) TOPOLOGY: unknown

(vi)

ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: D3

5

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO:61:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	Gln	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Met	Ile	Met	
					20					25					30	
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asp	Asn	Ser	Ser	
					35					40					45	
10	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ser	
					50					55					60	
	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	
					65					70					75	
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85					90	
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	
					95					100					105	
15	Arg	His	Glu	Thr	Val	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115					120	
	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Ala	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	
					140					145					150	
	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
20					155					160					165	
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	
					170					175					180	
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly				
					185					190						

25

(2) INFORMATION FOR SEQ ID NO:62:

(i)

SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

30

(vi)

ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: DK1

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO:62:

35

Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
				5					10					15	

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Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Val Asp Val Ile Met
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn His Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
 50 55 60
 5 Ser Ile Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Glu Thr Ala Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 10 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Leu Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Ala Gly Asn Trp Ala Lys Val
 170 175 180
 15 Leu Ile Val Leu Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 25 (C) INDIVIDUAL ISOLATE: HK3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Val Val Tyr Glu Thr Ala Asp Met Ile Met
 20 25 30
 30 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Val
 50 55 60
 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 35

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Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Leu Tyr Pro Gly
 110 115 120
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 5 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

10

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 15 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

20 His Glu Val His Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
 35 40 45
 25 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
 50 55 60
 Ser Ile Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 30 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Leu Pro
 140 145 150
 Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 35

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° Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:65:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 15 Cys Ser Asn Leu Ser Ile Val Tyr Glu Thr Thr Asp Met Ile Met
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Ala Pro Thr Leu Ala Ala Arg Asn Ala
 50 55 60
 Ser Val Pro Thr Thr Ala Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 20 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 25 Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190
 30

(2) INFORMATION FOR SEQ ID NO:66:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown

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(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: HK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

5 Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met
 20 25 30
 His Thr Pro Gly Cys Met Pro Cys Val Arg Glu Asn Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Val
 50 55 60
 10 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 15 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Ile Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 20 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:67:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 30 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

35 Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
 20 25 30

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5 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
 50 55 60
 Ser Val Ser Thr Thr Thr Ile Arg His His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 10 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Ile Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190
 15

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

25 Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Phe Ser
 35 40 45
 30 Ser Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
 50 55 60
 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 35

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° Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Ile Leu
 155 160 165
 5 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:69:

10

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: P10

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 20 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ser
 50 55 60
 Ser Val Pro Thr Thr Ala Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 25 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Leu Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Trp Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 30 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Ile Leu Asp Val Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 35 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

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(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

10	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Ala	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Val	Ile	Met
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Gln	Glu	Gly	Asn	Ser	Ser
					35					40					45
	Gln	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala
15					50					55					60
	Thr	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ala	Ala	Val	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Ile	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg
					95					100					105
20	Arg	His	Glu	Thr	Val	Gln	Asn	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Val	Met	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
25	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
					185					190					

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens

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(C) INDIVIDUAL ISOLATE: S45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Ala	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
5	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Val	Asp	Val	Ile	Leu
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ser
					50					55					60
	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75
10	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
15	Ser	Pro	Thr	Ala	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
20					185					190					

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

30	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser
					35					40					45
35	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ser
					50					55					60

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Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 5 Arg Tyr Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 Arg Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Ile Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 10 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:73:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 25 Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Ala Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Thr
 50 55 60
 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 30 Gly Ala Ala Ala Phe Cys Ser Val Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 35 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135

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Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 5 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 10 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T3

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr Tyr Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Ser Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
 50 55 60
 Ser Val Pro Thr Lys Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 25 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 30 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Leu Leu Leu Phe Ala Gly Val Asp Gly
 185 190

35

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° (2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

10	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	5	10	15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Phe	Glu	Ala	Ala	Asp	Leu	Ile	Met	20	25	30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ser	Ser	35	40	45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Thr	50	55	60
15	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	65	70	75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	80	85	90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	95	100	105
	Arg	His	Glu	Thr	Leu	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	110	115	120
20	His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	125	130	135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	140	145	150
	Gln	Ala	Val	Met	Asp	Met	Val	Thr	Gly	Ala	His	Trp	Gly	Val	Leu	155	160	165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Ala	Gly	Asn	Trp	Ala	Lys	Val	170	175	180
25	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly				185	190	

(2) INFORMATION FOR SEQ ID NO:76:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US6

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Tyr Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
 20 25 30
 5 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
 50 55 60
 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Thr Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 10 Gly Ser Val Phe Leu Ile Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Gln His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 15 Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Leu Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ala Gln Val Arg Asn Thr Ser Arg Gly Tyr Met Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Glu Ser Ile Thr Trp Gln Leu Gln Ala Ala Val Leu
 20 25 30
 His Val Pro Gly Cys Ile Pro Cys Glu Arg Leu Gly Asn Thr Ser
 35 40 45
 Arg Cys Trp Ile Pro Val Thr Pro Asn Val Ala Val Arg Gln Pro
 50 55 60

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°	Gly	Ala	Leu	Thr	Gln	Gly	Leu	Arg	Thr	His	Ile	Asp	Met	Val	Val
					65					70					75
	Met	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Gly	Val	Met	Leu	Ala	Ala	Gln	Met	Phe	Ile	Val	Ser	Pro	Arg
					95					100					105
	Arg	His	Trp	Phe	Val	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
5	Thr	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Ala	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Met	Arg	Val	Pro
					140					145					150
	Glu	Val	Ile	Ile	Asp	Ile	Ile	Gly	Gly	Ala	His	Trp	Gly	Val	Met
					155					160					165
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val
10					170					175					180
	Ile	Val	Ile	Leu	Leu	Leu	Ala	Ala	Gly	Val	Asp	Ala			
					185					190					

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: T4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

	Ala	Gln	Val	Lys	Asn	Thr	Thr	Asn	Ser	Tyr	Met	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Asp	Ser	Ile	Thr	Trp	Gln	Leu	Gln	Ala	Ala	Val	Leu
					20					25					30
25	His	Val	Pro	Gly	Cys	Val	Pro	Cys	Glu	Lys	Thr	Gly	Asn	Thr	Ser
					35					40					45
	Arg	Cys	Trp	Ile	Pro	Val	Ser	Pro	Asn	Val	Ala	Val	Arg	Gln	Pro
					50					55					60
	Gly	Ala	Leu	Thr	Gln	Gly	Leu	Arg	Thr	His	Ile	Asp	Met	Val	Val
					65					70					75
	Met	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
30	Gly	Gly	Val	Met	Leu	Ala	Ala	Gln	Met	Phe	Ile	Val	Ser	Pro	Gln
					95					100					105
	His	His	Trp	Phe	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	Thr	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Ala	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Met	Arg	Val	Pro
35					140					145					150

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Glu Val Ile Leu Asp Ile Val Ser Gly Ala His Trp Gly Val Met
 155 160 165
 Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
 170 175 180
 Val Val Ile Leu Leu Leu Ala Ala Gly Val Asp Ala
 185 190

5

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

15 Ala Glu Val Lys Asn Thr Ser Thr Ser Tyr Met Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Asp Ser Ile Thr Trp Gln Leu Gln Ala Ala Val Leu
 20 25 30
 His Val Pro Gly Cys Val Pro Cys Glu Arg Val Gly Asn Ala Ser
 35 40 45
 Arg Cys Trp Ile Pro Val Ser Pro Asn Val Ala Val Gln Arg Pro
 50 55 60
 Gly Ala Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val
 65 70 75
 Met Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Gly Val Met Leu Ala Ala Gln Met Phe Ile Ile Ser Pro Gln
 95 100 105
 25 His His Trp Phe Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 Thr Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Thr Met Ile Leu Ala Tyr Ala Met Arg Val Pro
 140 145 150
 Glu Val Ile Ile Asp Ile Ile Ser Gly Ala His Trp Gly Val Met
 155 160 165
 30 Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
 170 175 180
 Val Val Ile Leu Leu Leu Thr Ala Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:80:

35

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: US10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

	Val	Gln	Val	Lys	Asn	Thr	Ser	Thr	Ser	Tyr	Met	Val	Thr	Asn	Asp	
					5					10						15
	Cys	Ser	Asn	Asp	Ser	Ile	Thr	Trp	Gln	Leu	Glu	Ala	Ala	Val	Leu	
10					20					25						30
	His	Val	Pro	Gly	Cys	Val	Pro	Cys	Glu	Lys	Val	Gly	Asn	Thr	Ser	
					35					40						45
	Arg	Cys	Trp	Ile	Pro	Val	Ser	Pro	Asn	Val	Ala	Val	Gln	Arg	Pro	
					50					55						60
	Gly	Ala	Leu	Thr	Gln	Gly	Leu	Arg	Thr	His	Ile	Asp	Met	Val	Val	
					65					70						75
15	Met	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Phe	Cys	
					80					85						90
	Gly	Gly	Met	Met	Leu	Ala	Ala	Gln	Met	Phe	Ile	Val	Ser	Pro	Arg	
					95					100						105
	His	His	Ser	Phe	Val	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115						120
	Thr	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130						135
20	Ser	Pro	Thr	Ala	Thr	Leu	Ile	Leu	Ala	Tyr	Val	Met	Arg	Val	Pro	
					140					145						150
	Glu	Val	Ile	Ile	Asp	Ile	Ile	Ser	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160						165
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val	
					170					175						180
	Val	Val	Ile	Leu	Leu	Leu	Ala	Ala	Gly	Val	Asp	Ala				
25					185					190						

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: DK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

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	Val	Glu	Val	Arg	Asn	Ile	Ser	Ser	Ser	Tyr	Tyr	Ala	Thr	Asn	Asp	
					5					10					15	
	Cys	Ser	Asn	Asn	Ser	Ile	Thr	Trp	Gln	Leu	Thr	Asp	Ala	Val	Leu	
					20					25					30	
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Glu	Asn	Asp	Asn	Gly	Thr	Leu	
					35					40					45	
5	Arg	Cys	Trp	Ile	Gln	Val	Thr	Pro	Asn	Val	Ala	Val	Lys	His	Arg	
					50					55					60	
	Gly	Ala	Leu	Thr	His	Asn	Leu	Arg	Thr	His	Val	Asp	Val	Ile	Val	
					65					70					75	
	Met	Ala	Ala	Thr	Val	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Val	Cys	
					80					85					90	
	Gly	Ala	Val	Met	Ile	Val	Ser	Gln	Ala	Leu	Ile	Ile	Ser	Pro	Glu	
					95					100					105	
10	Arg	His	Asn	Phe	Thr	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Gln	Gly	
					110					115					120	
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Leu	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Leu	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Ala	Arg	Val	Pro	
					140					145					150	
	Glu	Leu	Ala	Leu	Gln	Val	Val	Phe	Gly	Gly	His	Trp	Gly	Val	Val	
					155					160					165	
15	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val	
					170					175					180	
	Ile	Ala	Ile	Leu	Leu	Leu	Val	Ala	Gly	Val	Asp	Ala				
					185					190						

(2) INFORMATION FOR SEQ ID NO:82:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

25

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

	Val	Glu	Val	Arg	Asn	Thr	Ser	Ser	Ser	Tyr	Tyr	Ala	Thr	Asn	Asp
					5					10					15
30	Cys	Ser	Asn	Asn	Ser	Ile	Thr	Trp	Gln	Leu	Thr	Asn	Ala	Val	Leu
					20					25					30
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Glu	Asn	Asp	Asn	Gly	Thr	Leu
					35					40					45
	His	Cys	Trp	Ile	Gln	Val	Thr	Pro	Asn	Val	Ala	Val	Lys	His	Arg
					50					55					60
	Gly	Ala	Leu	Thr	His	Asn	Leu	Arg	Ala	His	Ile	Asp	Met	Ile	Val
35					65					70					75

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° Met Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
 80 85 90
 Gly Ala Val Met Ile Val Ser Gln Ala Phe Ile Val Ser Pro Glu
 95 100 105
 His His His Phe Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly
 110 115 120
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp
 125 130 135
 5 Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro
 140 145 150
 Glu Leu Val Leu Glu Val Val Phe Gly Gly His Trp Gly Val Val
 155 160 165
 Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
 170 175 180
 10 Ile Ala Ile Leu Leu Leu Val Ala Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW3

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Val Glu Val Arg Asn Ile Ser Ser Ser Tyr Tyr Ala Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Thr Trp Gln Leu Thr Asn Ala Val Leu
 20 25 30
 His Leu Pro Gly Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu
 35 40 45
 25 His Cys Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg
 50 55 60
 Gly Ala Leu Thr His Asn Leu Arg Ala His Val Asp Met Ile Val
 65 70 75
 Met Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Met Cys
 80 85 90
 Gly Ala Val Met Ile Val Ser Gln Ala Phe Ile Ile Ser Pro Glu
 95 100 105
 30 Arg His Asn Phe Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly
 110 115 120
 Arg Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp
 125 130 135
 Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro
 140 145 150
 35 Glu Leu Val Leu Glu Val Val Phe Gly Gly His Trp Gly Val Val
 155 160 165

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Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
 170 175 180
 Ile Ala Ile Leu Leu Leu Val Ala Gly Val Asp Ala
 185 190

5 (2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

15 Val Glu Val Arg Asn Thr Ser Phe Ser Tyr Tyr Ala Thr Asn Asp
 5 10 15
 Cys Ser Asn Asn Ser Ile Thr Trp Gln Leu Thr Asn Ala Val Leu
 20 25 30
 His Leu Pro Gly Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu
 35 40 45
 Arg Cys Trp Ile Gln Val Thr Pro Asn Val Ala Val Lys His Arg
 50 55 60
 20 Gly Ala Leu Thr His Asn Leu Arg Thr His Val Asp Val Ile Val
 65 70 75
 Met Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
 80 85 90
 Gly Ala Val Met Ile Ala Ser Gln Ala Phe Ile Ile Ser Pro Glu
 95 100 105
 Arg His Asn Phe Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly
 110 115 120
 25 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Leu Asn Trp
 125 130 135
 Ser Pro Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro
 140 145 150
 Glu Leu Val Leu Glu Val Val Phe Gly Gly His Trp Gly Val Val
 155 160 165
 Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val
 170 175 180
 30 Ile Ala Ile Leu Leu Leu Val Ala Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:85:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids

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(B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

	Val	Glu	Val	Lys	Asp	Thr	Gly	Asp	Ser	Tyr	Met	Pro	Thr	Asn	Asp	
					5					10					15	
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Trp	Gln	Leu	Glu	Gly	Ala	Val	Leu	
					20					25					30	
10	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Glu	Arg	Thr	Ala	Asn	Val	Ser	
					35					40					45	
	Arg	Cys	Trp	Val	Pro	Val	Ala	Pro	Asn	Leu	Ala	Ile	Ser	Gln	Pro	
					50					55					60	
	Gly	Ala	Leu	Thr	Lys	Gly	Leu	Arg	Ala	His	Ile	Asp	Ile	Ile	Val	
					65					70					75	
	Met	Ser	Ala	Thr	Val	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Val	Cys	
					80					85					90	
15	Gly	Ala	Leu	Met	Leu	Ala	Ala	Gln	Val	Val	Val	Val	Ser	Pro	Gln	
					95					100					105	
	His	His	Thr	Phe	Val	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115					120	
	Arg	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Thr	Thr	Met	Leu	Leu	Ala	Tyr	Leu	Val	Arg	Ile	Pro	
					140					145					150	
20	Glu	Val	Ile	Leu	Asp	Ile	Val	Thr	Gly	Gly	His	Trp	Gly	Val	Met	
					155					160					165	
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ser	Trp	Ala	Lys	Val	
					170					175					180	
	Ile	Val	Ile	Leu	Leu	Leu	Thr	Ala	Gly	Val	Glu	Ala				
					185					190						

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

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0 Leu Glu Trp Arg Asn Val Ser Gly Leu Tyr Val Leu Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser
 35 40 45
 Thr Cys Trp Thr Ser Val Thr Pro Thr Val Ala Val Arg Tyr Val
 50 55 60
 5 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
 80 85 90
 Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg
 95 100 105
 10 Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly
 110 115 120
 His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Ala Val Gly Met Val Val Ala His Val Leu Arg Leu Pro
 140 145 150
 Gln Thr Leu Phe Asp Ile Ile Ala Gly Ala His Trp Gly Ile Met
 155 160 165
 15 Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val
 170 175 180
 Ala Ile Ile Met Val Met Phe Ser Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:87:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 25 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Leu Glu Trp Arg Asn Val Ser Gly Leu Tyr Val Leu Thr Asn Asp
 5 10 15
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu
 20 25 30
 30 His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser
 35 40 45
 Thr Cys Trp Thr Ser Val Thr Pro Thr Val Ala Val Arg Tyr Val
 50 55 60
 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
 65 70 75
 35 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys
 80 85 90

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Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg
 95 100 105
 Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly
 110 115 120
 His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 5 Ser Pro Ala Val Gly Met Val Val Ala His Val Leu Arg Leu Pro
 140 145 150
 Gln Thr Leu Phe Asp Ile Ile Ala Gly Ala His Trp Gly Ile Leu
 155 160 165
 Ala Gly Leu Ala Tyr Ser Met Gln Gly Asn Trp Ala Lys Val
 170 175 180
 Ala Ile Ile Met Val Met Phe Ser Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

20 Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser
 35 40 45
 25 Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
 50 55 60
 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys
 80 85 90
 Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg
 95 100 105
 30 Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly
 110 115 120
 His Leu Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Ala Val Gly Met Val Val Ala His Val Leu Arg Leu Pro
 140 145 150
 Gln Thr Val Phe Asp Ile Ile Ala Gly Ala His Trp Gly Ile Leu
 155 160 165

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° Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val
 170 175 180
 Ala Ile Ile Met Val Met Phe Ser Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:89:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

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- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S52

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu Thr Asn Asp
 5 10 15
 15 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser
 35 40 45
 Met Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
 50 55 60
 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
 65 70 75
 20 Gly Ala Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Met Cys
 80 85 90
 Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg
 95 100 105
 Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly
 110 115 120
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 25 Ser Pro Ala Val Gly Met Val Val Ala His Ile Leu Arg Leu Pro
 140 145 150
 Gln Thr Leu Phe Asp Ile Leu Ala Gly Ala His Trp Gly Ile Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val
 170 175 180
 Ala Ile Val Met Ile Met Phe Ser Gly Val Asp Ala
 185 190
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(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown

35

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(D) TOPOLOGY: unknown

(vi)

ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: S54

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO:90:

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Leu	Glu	Trp	Arg	Asn	Thr	Ser	Gly	Leu	Tyr	Ile	Leu	Thr	Asn	Asp
				5					10					15
Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Val	Ile	Leu
				20					25					30
His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Gln	Asp	Gly	Asn	Thr	Ser
				35					40					45
Thr	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	Ala	Val	Arg	Tyr	Val
				50					55					60
Gly	Ala	Thr	Thr	Ala	Ser	Ile	Arg	Ser	His	Val	Asp	Leu	Leu	Val
				65					70					75
Gly	Ala	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Met	Cys
				80					85					90
Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Ala	Phe	Thr	Phe	Arg	Pro	Arg
				95					100					105
Arg	His	Gln	Thr	Val	Gln	Thr	Cys	Asn	Cys	Ser	Leu	Tyr	Pro	Gly
				110					115					120
His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
				125					130					135
Ser	Pro	Ala	Val	Gly	Met	Val	Val	Ala	His	Ile	Leu	Arg	Leu	Pro
				140					145					150
Gln	Thr	Leu	Phe	Asp	Ile	Leu	Ala	Gly	Ala	His	Trp	Gly	Ile	Leu
				155					160					165
Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Gln	Gly	Asn	Trp	Ala	Lys	Val
				170					175					180
Ala	Ile	Ile	Met	Ile	Met	Phe	Ser	Gly	Val	Asp	Ala			
				185					190					

(2) INFORMATION FOR SEQ ID NO:91:

(i)

SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi)

ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: Z4

(xi)

SEQUENCE DESCRIPTION: SEQ ID NO:91:

Glu	His	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Ile	Thr	Asn	Asp
				5					10					15

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0	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	His	His	Ile	Leu
					20					25					30
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Met	Thr	Gly	Asn	Thr	Ser
					35					40					45
	Arg	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	Ala	Val	Ala	His	Pro
					50					55					60
	Gly	Ala	Pro	Leu	Glu	Ser	Phe	Arg	Arg	His	Val	Asp	Leu	Met	Val
					65					70					75
5	Gly	Ala	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Gly	Ala	Phe	Leu	Met	Gly	Gln	Met	Ile	Thr	Phe	Arg	Pro	Arg
					95					100					105
	Arg	His	Trp	Thr	Thr	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Thr	Gly
					110					115					120
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
10					125					130					135
	Ser	Pro	Thr	Thr	Thr	Leu	Leu	Leu	Ala	Gln	Ile	Met	Arg	Val	Pro
					140					145					150
	Thr	Ala	Phe	Leu	Asp	Met	Val	Ala	Gly	Gly	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
15	Val	Leu	Val	Leu	Phe	Leu	Phe	Ala	Gly	Val	Asp	Ala			
					185					190					

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

	Val	His	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Pro	Asn	Thr	Ser	Ile	Val	Tyr	Glu	Thr	Glu	His	His	Ile	Met	
					20					25					30	
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Thr	Glu	Asn	Thr	Ser	
					35					40					45	
	Arg	Cys	Trp	Val	Pro	Leu	Thr	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Pro	
					50					55					60	
	Asn	Ala	Pro	Leu	Glu	Ser	Met	Arg	Arg	His	Val	Asp	Leu	Met	Val	
					65					70					75	
	Gly	Ala	Ala	Thr	Met	Cys	Ser	Ala	Phe	Tyr	Ile	Gly	Asp	Leu	Cys	
					80					85					90	
	Gly	Gly	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Asp	Phe	Arg	Pro	Arg	
					95					100					105	

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Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ser Ala Leu Ile Met Ala Gln Ile Leu Arg Ile Pro
 140 145 150
 5 Ser Ile Leu Gly Asp Leu Leu Thr Gly Gly His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Phe Phe Ser Met Gln Ser Asn Trp Ala Lys Val
 170 175 180
 Ile Leu Val Leu Phe Leu Phe Ala Gly Val Glu Gly
 185 190

10 (2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Glu His Gln Ile Leu
 20 25 30
 His Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Val Ala Val Ser Tyr Ile
 50 55 60
 25 Gly Ala Pro Leu Asp Ser Leu Arg Arg His Val Asp Leu Met Val
 65 70 75
 Gly Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Gly Ala Phe Leu Val Gly Gln Met Phe Ser Phe Gln Pro Arg
 95 100 105
 Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Ala Gly
 110 115 120
 30 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Thr Leu Leu Leu Ala Gln Val Met Arg Ile Pro
 140 145 150
 Ser Thr Leu Val Asp Leu Leu Ala Gly Gly His Trp Gly Val Leu
 155 160 165
 Val Gly Leu Ala Tyr Phe Ser Met Gln Ala Asn Trp Ala Lys Val
 170 175 180

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Ile Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z7

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

	Val	Asn	Tyr	His	Asn	Ala	Ser	Gly	Val	Tyr	His	Ile	Thr	Asn	Asp	
					5					10					15	
	Cys	Pro	Asn	Ser	Ser	Ile	Met	Tyr	Glu	Ala	Glu	His	His	Ile	Leu	
					20					25					30	
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Gln	Ser	
					35					40					45	
15	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Ile	
					50					55					60	
	Gly	Ala	Pro	Leu	Glu	Ser	Ile	Arg	Arg	His	Val	Asp	Leu	Met	Val	
					65					70					75	
	Gly	Ala	Ala	Thr	Val	Cys	Ser	Ala	Leu	Tyr	Ile	Gly	Asp	Leu	Cys	
					80					85					90	
	Gly	Gly	Val	Phe	Leu	Val	Gly	Gln	Met	Phe	Ser	Phe	Gln	Pro	Arg	
20					95					100					105	
	Arg	His	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Ala	Gly	
					110					115					120	
	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Thr	Thr	Leu	Val	Leu	Ala	Gln	Val	Met	Arg	Ile	Pro	
					140					145					150	
25	Ser	Thr	Leu	Val	Asp	Leu	Leu	Thr	Gly	Gly	His	Trp	Gly	Ile	Leu	
					155					160					165	
	Ile	Gly	Val	Ala	Tyr	Phe	Cys	Met	Gln	Ala	Asn	Trp	Ala	Lys	Val	
					170					175					180	
	Ile	Leu	Val	Leu	Phe	Leu	Tyr	Ala	Gly	Val	Asp	Ala				
					185					190						

30 (2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

35 (vi) ORIGINAL SOURCE:

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(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

5	Tyr	Asn	Tyr	Arg	Asn	Ser	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	15
					5					10						
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Asp	Tyr	His	Ile	Leu	30
					20					25						
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Lys	Ser	45
					35					40						
	Thr	Cys	Trp	Val	Ser	Leu	Thr	Pro	Thr	Val	Ala	Ala	Gln	His	Leu	60
					50					55						
10	Asn	Ala	Pro	Leu	Glu	Ser	Leu	Arg	Arg	His	Val	Asp	Leu	Met	Val	75
					65					70						
	Gly	Gly	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Ile	Gly	Asp	Val	Cys	90
					80					85						
	Gly	Gly	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Gln	Pro	Arg	105
					95					100						
	Arg	His	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Thr	Gly	120
					110					115						
15	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	135
					125					130						
	Ser	Pro	Thr	Ala	Thr	Leu	Val	Leu	Ala	Gln	Leu	Met	Arg	Ile	Pro	150
					140					145						
	Gly	Ala	Met	Val	Asp	Leu	Leu	Ala	Gly	Gly	His	Trp	Gly	Ile	Leu	165
					155					160						
	Val	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Gln	Ala	Asn	Trp	Ala	Lys	Val	180
20					170					175						
	Ile	Leu	Val	Leu	Phe	Leu	Phe	Ala	Gly	Val	Asp	Ala				190
					185					190						

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

35	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	15
					5					10						
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Ser	Leu	Ile	Leu	30
					20					25						
	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Gln	Asp	Asn	Val	Ser	45
					35					40						

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Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Thr Phe
 50 55 60
 Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
 65 70 75
 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
 80 85 90
 5 Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg
 95 100 105
 Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
 110 115 120
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Leu Met Ala Gln Met Leu Arg Ile Pro
 140 145 150
 10 Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
 155 160 165
 Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
 170 175 180
 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Gly
 185 190

15 (2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

25 Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu
 20 25 30
 His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Asp Asn Val Ser
 35 40 45
 Lys Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Asn Leu
 50 55 60
 30 Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
 65 70 75
 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
 80 85 90
 Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg
 95 100 105
 Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
 110 115 120

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° His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Leu Met Ala Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
 155 160 165
 Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
 170 175 180
 5 Ile Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 15 (C) INDIVIDUAL ISOLATE: SAS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	
					20					25					30	
20	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Lys	Glu	Gly	Asn	Val	Ser	
					35					40					45	
	Arg	Cys	Trp	Val	Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Asn	Leu	
					50					55					60	
	Gly	Ala	Val	Thr	Ala	Pro	Leu	Arg	Arg	Val	Val	Asp	Tyr	Leu	Ala	
					65					70					75	
	Gly	Gly	Ala	Ala	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	
					80					85					90	
25	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Met	Phe	Thr	Tyr	Arg	Pro	Arg	
					95					100					105	
	Gln	His	Thr	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Ser	Gly	
					110					115					120	
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Met	Ala	Gln	Val	Leu	Arg	Ile	Pro	
					140					145					150	
30	Gln	Val	Val	Ile	Asp	Ile	Ile	Ala	Gly	Gly	His	Trp	Gly	Val	Leu	
					155					160					165	
	Phe	Ala	Val	Ala	Tyr	Phe	Ala	Ser	Ala	Ala	Asn	Trp	Ala	Lys	Val	
					170					175					180	
	Val	Leu	Val	Leu	Phe	Leu	Phe	Ala	Gly	Val	Asp	Gly				
					185					190						

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° (2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

10	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	5	10	15
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Leu	Ile	Leu	20	25	30
	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Lys	Asp	Asn	Val	Ser	35	40	45
	Arg	Cys	Trp	Val	His	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Ser	Leu	50	55	60
15	Gly	Ala	Val	Thr	Ala	Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Ala	65	70	75
	Gly	Gly	Ala	Ala	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Val	Cys	80	85	90
	Gly	Ala	Leu	Phe	Leu	Val	Gly	Gln	Met	Phe	Thr	Tyr	Arg	Pro	Arg	95	100	105
	Gln	His	Ala	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Ser	Gly	110	115	120
20	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	125	130	135
	Ser	Pro	Ala	Thr	Ala	Leu	Val	Met	Ala	Gln	Met	Leu	Arg	Ile	Pro	140	145	150
	Gln	Val	Val	Ile	Asp	Ile	Ile	Ala	Gly	Gly	His	Trp	Gly	Val	Leu	155	160	165
	Phe	Ala	Ala	Ala	Tyr	Phe	Ala	Ser	Ala	Ala	Asn	Trp	Ala	Lys	Val	170	175	180
25	Val	Leu	Val	Leu	Phe	Leu	Phe	Ala	Gly	Val	Asp	Ala				185	190	

(2) INFORMATION FOR SEQ ID NO:100:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA7

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu
 20 25 30
 5 His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Asn Asn Val Ser
 35 40 45
 Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Asn Leu
 50 55 60
 Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
 65 70 75
 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
 80 85 90
 10 Gly Ala Val Phe Leu Val Gly Gln Met Phe Ser Tyr Arg Pro Arg
 95 100 105
 Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
 110 115 120
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro
 140 145 150
 15 Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
 155 160 165
 Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
 170 175 180
 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu
 20 25 30
 30 His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Gly Asn Val Ser
 35 40 45
 Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu
 50 55 60

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° Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
65 70 75
Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
80 85 90
Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Ser Pro Arg
95 100 105
Arg His Asn Val Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
110 115 120
5 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Thr Thr Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro
140 145 150
Gln Val Val Ile Asp Ile Ile Ala Gly Ala His Trp Gly Val Leu
155 160 165
Phe Ala Ala Ala Tyr Tyr Ala Ser Ala Ala Asn Trp Ala Lys Val
170 175 180
10 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:102:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
20 (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Leu Thr Tyr Gln Asn Ser Ser Gln Leu Tyr His Leu Thr Asn Asp
1 10 15
Cys Pro Asn Ser Ser Ile Val Leu Glu Ala Asp Ala Met Ile Leu
20 25 30
25 His Leu Pro Gln Cys Leu Pro Cys Val Arg Val Asp Asp Arg Ser
35 40 45
Thr Cys Trp His Ala Val Thr Pro Thr Leu Ala Ile Pro Asn Ala
50 55 60
Ser Thr Pro Ala Thr Gln Phe Arg Arg His Val Asp Leu Leu Ala
65 70 75
Gln Ala Ala Val Val Cys Ser Ser Leu Tyr Ile Gln Asp Leu Cys
80 85 90
30 Gln Ser Leu Phe Leu Ala Gln Gln Leu Phe Thr Phe Gln Pro Arg
95 100 105
Arg His Trp Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Thr Gln
110 115 120
His Val Thr Gln His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
35 Ser Pro Thr Thr Thr Leu Val Leu Ser Ser Ile Leu Arg Val Pro
140 145 150

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Glu Ile Cys Ala Ser Val Ile Phe Gln Gln His Trp Gln Ile Leu
 155 160 165
 Leu Ala Val Ala Tyr Phe Gln Met Ala Gln Asn Trp Leu Lys Val
 170 175 180
 Leu Ala Val Leu Phe Leu Phe Ala Gln Val Glu Ala
 185 190

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(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

15 ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
 AAC ACC AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGT 78
 GGC GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC 117
 AGG GGC CCT AGA TTG GGT GTG CGC GCG CCG AGG AAG ACT 156
 TCC GAG CGG TCG CAA CCT CGA GGT AGA CGT CAG CCT ATC 195
 CCC AAG GCA CGT CGG CCC GAG GGC AGG ACC TGG GCT CAG 234
 CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TGC 273
 20 GGG TGG GCG GGA TGG CTC CTG TCT CCC CGT GGC TCT CGG 312
 CCT AGC TGG GGC CCC ACA GAC CCC CGG CGC AGG TCG CGC 351
 AAT TTG GGT AAA GTC ATC GAT ACC CTT ACG TGC GGC TTC 390
 GCC GAC CTC ATG GGG TAC ATA CCG CTC GTC GGC GCC CCT 429
 CTT GGA GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG 468
 GTT CTG GAA GAC GGC GTG AAC TAT GCA ACA GGG AAC CTT 507
 CCT GGT TGC TCT TTC TCT ATC TTC CTT TTG GCC CTG CTC 546
 25 TCT TGC CTG ACC GTG CCC GCT TCG GCC 573

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

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(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

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(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SW1

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	78
	GGC	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCT	AGA	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAG	ACT	156
	TCC	GAG	CGG	TCG	CAA	CCT	CGA	GGT	AGA	CGT	CAG	CCT	ATC	195
10	CCC	AAG	GCG	CGT	CGG	CCC	GAG	GGC	AGG	ACC	TGG	GCT	CAG	234
	CCC	GGG	TAT	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TGC	273
	GGA	TGG	GCG	GGA	TGG	CTC	CTG	TCC	CCC	CGT	GGC	TCT	CGG	312
	CCT	AGC	TGG	GGC	CCT	ACA	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGC	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCT	429
	CTT	GGA	GGC	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	468
15	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	CTT	507
	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	CTG	GCC	CTG	CTT	546
	TCT	TGC	CTG	ACA	GTG	CCC	GCG	TCA	GCC					573

(2) INFORMATION FOR SEQ ID NO: 107:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S18

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

	ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGT	78
	GGC	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCT	AGA	TTG	GGT	GTG	GCG	ACG	AGG	AAG	ACT		156
30	TCC	GAG	CGG	TCG	CAA	CCT	CGC	GGT	AGA	CGT	CAG	CCT	ATC	195
	CCC	AAG	GCG	CGT	CGG	CCC	GAG	GGC	AGG	ACC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TGC	273
	GGG	TGG	GCG	GGA	TGG	CTC	CTG	TCC	CCC	CGT	GGC	TCC	CGG	312
	CCT	AGC	TGG	GGC	CCT	ACA	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
	AAT	TTG	GGC	AAA	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGC	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCT	429
35	CTC	GGA	GGC	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	468
	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	CTT	507

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CCT GGT TGC TCT TTC TCT ATC TTC CTT CTG GCC CTG CTC 546
TCT TGT CTG ACT GTG CCC GCG TCA GCT 573

(2) INFORMATION FOR SEQ ID NO: 108:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
10 (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DR4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	78
	GGC	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
15	AGG	GGC	CCT	AGA	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAG	ACT	156
	TCC	GAG	CGG	TCG	CAA	CCT	CGA	GGT	AGA	CGT	CAG	CCT	ATC	195
	CCC	AAG	GCG	CGT	CGG	CCC	GAG	GGC	AGG	ACC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TGC	273
	GGG	TGG	GCG	GGA	TGG	CTC	CTG	TCC	CCC	CGT	GGC	TCT	CGG	312
	CCT	AGC	TGG	GGC	CCC	ACA	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAC	ACC	CTC	ACG	TGC	GGC	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTC	GGC	GCC	CCC	429
20	CTT	GGG	GGC	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGA	468
	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	CTT	507
	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	TTG	GCT	TTG	CTC	546
	TCT	TGC	TTG	ACC	GTG	CCC	GCA	TCG	GCC					573

(2) INFORMATION FOR SEQ ID NO: 109:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
30 (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTC	TAT	CTG	TTG	CCG	CGC	117
35	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAG	ACT	156

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TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC 195
 CCC AAG GCT CGC CAG CCC GAG GGC AGG ACC TGG GCC CAG 234
 CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TTG 273
 GGG TGG GCA GGA TGG CTC CTG TCA CCC CGT GGC TCT CGG 312
 CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGT 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
 5 GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCT 429
 TTA GGG GGC GCT GCC AGG GCC TTG GCG CAT GGC GTC CGG 468
 GTT CTG GAA GAC GGC GTG AAC TAT GCA ACA GGG AAT TTG 507
 CCC GGT TGC CCT TTC TCT ATC TTC CTC TTG GCT TTG CTG 546
 TCC TGT TTA ACC ATC CCA GCT TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 110:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S45

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

ATG AGC ACG AAT CCT AAA CCT CAA AGA CAA ACC AAA CGT 39
 AAC ACC AAC ACG CGC CCA CAG GAC GTC AAG TTC CCG GGT 78
 20 GGC GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC 117
 AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT 156
 TCC GAG CGG TCA CAA CCT CGT GGA CGG CGA CAA CCT ATC 195
 CCC AAG GCT CGC CGG CCC GAG GGC AGG GCC TGG GCC CAG 234
 CCC GGG CAT CCT TGG CCC CTC TAT GGC AAT GAG GGC TTG 273
 GGG TGG GCA GGA TGG CTC CTG TCA CCC CGT GGC TCC CGG 312
 CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGC 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTC ACG TGC GGC TTC 390
 25 GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC 429
 CTA GGG GGC GCT GCC AGA GCC TTG GCG CAT GGC GTC CGG 468
 GTT CTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAT CTG 507
 CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT CTG CTG 546
 TCC TGC TTG ACC ATC CCA GCT TCC GCT 573

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(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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- (vi) ORIGINAL SOURCE:

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(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: D1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
5	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	AGG	AAG	ACT	156
	TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
	CCC	AAG	GCT	CGC	CGG	CCC	GAG	GGT	AGG	GCC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAC	GAG	GGC	TTG	273
	GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGC	GGC	TCC	CGG	312
	CCT	AGT	TGG	GGC	CCC	ACC	GAC	CCC	CGG	CGT	AGG	TCG	CGT	351
10	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTC	GGC	GCC	CCC	429
	CTA	GGG	GGT	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	468
	GTT	CTG	GAG	GAC	GGC	GTG	AAT	TAT	GCA	ACA	GGG	AAT	TTG	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	CTG	546
	TCC	TGT	TTG	ACC	ATC	CCA	GCT	TCC	GCT					573

15 (2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
25	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	AGG	AAG	ACT	156
	TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
	CCC	AAG	GCT	CGC	CGG	CCC	GAG	GGC	AGG	GCC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAC	GAG	GGC	ATG	273
	GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGT	GGC	TCC	CGG	312
30	CCT	AGT	TGG	GGC	CCC	ACG	GAC	CCC	CGG	CGT	AGG	TCG	CGT	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	429
	CTA	GGG	GGC	GCT	GCC	AGG	GCC	TTG	GCG	CAT	GGC	GTC	CGG	468
	GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	TTG	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	CTG	546
	TCC	TGT	TTG	ACC	ATT	CCA	GCT	TCC	GCT					573

35

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(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: P10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

10	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT	156
	TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC	195
	CCC AAG GCT CGC CGG CCC GAG GGC AGG GCC TGG GCT CAG	234
	CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TTG	273
15	GGG TGG GCA GGA TGG CTC CTG TCA CCC CGT GGC TCT CGG	312
	CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGT	351
	AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC	390
	GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC	429
	CTA GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG	468
	GTT CTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAT CTG	507
	CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG CTG	546
20	TCC TGC CTG ACC ATC CCA GCG TCC GCT	573

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

30	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT	156
	TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC	195
	CCC AAG GCT CGC CGG CCC GAG GGC AGG GCC TGG GCT CAG	234
35	CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG	273
	GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGC TCT CGG	312

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CCT AGT TGG GGC CCC AAC GAC CCC CGG CGT AGG TCG CGT 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
 GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC 429
 CTA GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG 468
 GTT CTG GAG GAC GGC GTG AAC TAC GCA ACA GGG AAT TTG 507
 CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT CTG TTG 546
 TCC TGT TTG ACC ATC CCA GCT TCC GCC 573

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
 AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC 78
 GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC 117
 AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT 156
 TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAG CCT ATC 195
 CCC AAG GCT CGC CAG CCC GAG GGC AGG GCC TGG GCT CAG 234
 CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG 273
 GGG TGG GCA GGA TGG CTC CTG TCA CCC CGT GGC TCC CGG 312
 CCT AGT TGG GGC CCC ACA GAC CCC CGG CGT AGG TCG CGT 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
 GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC 429
 CTA GGG GGC GCT GCC AGG GCT CTG GCA CAT GGT GTC CGG 468
 GTT CTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAT TTG 507
 CCC GGT TGC TCT TTT TCT ATC TTC CTC TTG GCT CTG CTG 546
 TCT TGT CTG ACC ATC CCA GCT TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

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 10
 ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
 AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC 78
 GGT GGC CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC 117
 AGG GGC CCC CGG TTG GGT GTG CGC GCG ACT AGG AAG ACT 156
 TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC 195
 CCC AAG GCT CGC CAG CCC GAG GGC AGG GCC TGG GCT CAG 234
 CCT GGG TAC CCC TGG CCC CTC TAT GGC AAT GAG GGC ATG 273
 GGA TGG GCA GGA TGG CTC CTG TCC CCC CGC GGC TCT CGG 312
 CCT AGT TGG GGC CCC ACT GAC CCC CGG CGT AGG TCG CGT 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
 GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC 429
 CTA GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG 468
 GTC CTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAT CTG 507
 CCC GGT TGC TCC TTT TCT ATC TTC CTC TTG GCT TTG CTG 546
 TCC TGT CTG ACC ATC CCA GCT TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 117:

15
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND3

25
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

25
 30
 ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
 AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC 78
 GGT GGC CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC 117
 AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT 156
 TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC 195
 CCC AAG GCT CGC CGG CCC GAG GGT AGG GCC TGG GCT CAG 234
 CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TTG 273
 GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGT TCT CGG 312
 CCT AGT TGG GGC CCC ACA GAC CCC CGG CGT AGG TCG CGT 351
 AAT TTG GGT AAA GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
 GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCC CCC 429
 CTA GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG 468
 GTC CTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAC TTG 507
 CCC GGT TGC TCT TTC TCT ATC TTC CTT TTA GCT TTG CTA 546
 TCC TGT TTG ACC ATC CCA GCT TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 118:

35
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGC	CAG	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	AGG	AAG	ACT	156
10	TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
	CCC	AAG	GCT	CGC	CGG	CCC	GAG	GGT	AGG	GCC	TGG	GCT	CAG	234
	CCC	GGG	CAC	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TTG	273
	GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGC	GGC	TCT	CGG	312
	CCT	AGT	TGG	GGC	CCC	ACA	GAC	CCC	CGG	CGT	AGG	TCG	CGT	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTC	GGC	GCC	CCC	429
15	CTA	GGG	GGT	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	468
	GTC	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	TTG	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	TTG	GCT	TTG	CTA	546
	TCC	TGT	TTG	ACC	GTC	CCA	GCT	TCC	GCT					573

(2) INFORMATION FOR SEQ ID NO: 119:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTC	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
30	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCA	ACT	AGG	AAG	ACT	156
	TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
	CCC	AAG	GCT	CGC	CAT	CCC	GAG	GGC	AGG	GCC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAC	GGC	AAT	GAG	GGC	TTG	273
	GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGT	GGC	TCT	CGG	312
	CCT	AGT	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CGT	AGG	TCG	CGT	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	TTT	390
35	GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	429
	CTA	GGG	GGC	GCT	GCC	AGG	GCT	CTG	GCG	CAT	GGC	GTC	CGG	468

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GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	CTC	507
CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	CTG	GCT	TTG	CTG	546
TCC	TGT	TTG	ACC	ATC	CCA	GCT	TCC	GCT					573

(2) INFORMATION FOR SEQ ID NO: 120:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK3

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACC	AGG	AAG	ACT	156
TCA	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
CCC	AAG	GCT	CGC	CAA	CCC	GAG	GGC	AGG	ACC	TGG	GCT	CAG	234
CCC	GGG	TAT	CCT	TGG	CCC	CTC	TAT	GGC	AAC	GAG	GGC	ATG	273
GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGC	GGC	TCT	CGG	312
CCT	AAT	TGG	GGC	CCC	ACG	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTC	GGT	GCC	CCC	429
CTA	GGG	GGC	GTT	GCC	AGA	GCC	TTG	GCA	CAT	GGT	GTC	CGG	468
GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	TTA	507
CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	CTG	546
TCC	TGC	TTG	ACC	ACC	CCA	GCT	TCC	GCT					573

(2) INFORMATION FOR SEQ ID NO: 121:

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117

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AGG GGC CCC AGG TTG GGT GTG CGC GCG ACC AGG AAG ACT 156
 TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC 195
 CCC AAG GCT CGC CGA CCC GAG GGC AGG ACC TGG GCT CAG 234
 CCC GGG TAT CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG 273
 GGG TGG GCA GGA TGG CTC CTG TCA CCC CAT GGC TCT CGG 312
 CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGT 351
 5 AAT TTG GGT AAG GTC ATC GAT ACC CTC ACG TGC GGC TTC 390
 GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCC CCC 429
 CTA GGG GGC GTT GCC AGA GCC CTG GCA CAC GGT GTC CGG 468
 GTT CTG GAG GAC GGC GTG AAC TAC GCA ACA GGG AAT ATA 507
 CCC GGT TGC TCT TTC TCT ATC TTC CTT TTG GCT TTG CTG 546
 TCC TGT CTG ACC ACC CCA GTT TCC GCT 573

10 (2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

20 ATG AGC ACG AAT CCT AAA CCT CAA AGA AAG ACC AAA CGT 39
 AAC ACC AAC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGC 78
 GGT GGC CAG ATC GTC GGT GGA GTT TAC CTG TTG CCG CGC 117
 AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT 156
 TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC 195
 CCC AAG GCT CGC CAA CCC GAG GGC AGG ACC TGG GCT CAG 234
 CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG 273
 GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGC TCT CGG 312
 CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGC 351
 25 AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
 GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC 429
 TTA GGG GGC GTT GCC AGA GCC CTG GCA CAT GGT GTC CGG 468
 GTT GTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAT TTG 507
 CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT CTG CTG 546
 TCC TGT TTG ACC ATC CCA GCT TCC GCT 573

30 (2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 35 (D) TOPOLOGY: linear

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: P8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

5	ATG AGC ACG ACT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AGC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT	156
	TCC GAG CGA TCG CAA CCT CGT GGC AGG CGA CAA CCT ATC	195
	CCC AAG GCT CGC CGG CCC GAG GGT AGG GCC TGG GCT CAG	234
	CCC GGG CAC CCT TGG CCC CTC TAT GCC AAT GAG GGC TTG	273
	GGG TGG GCG GGA TGG CTC CTG TCA CCC CGC GGC TCC CGG	312
10	CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGC	351
	AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC	390
	GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GGC CCC	429
	CTA GGG GGC GTT GCC AGG GCC CTG GCG CAT GGC GTC CGG	468
	GTT GTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAT CTG	507
	CCT GGT TGC TCT TTC TCT ATC TTC CTT TTG GCT TTG CTG	546
	TCT TGT CTG ACC ATC CCA GCT TCC GCT	573

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

25	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT	156
	TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC	195
	CCC AAG GCT CGC CGG CCC GAG GGT AGG GCC TGG GCT CAG	234
	CCC GGG TAC CCT TGG CCC CTC TAT GGC GAC GAG GGC ATG	273
30	GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGC TCC CGG	312
	CCT AAT TGG GGC CCC ACA GAC CCC CGG CGT AGG TCG CGT	351
	AAT CTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC	390
	GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCT CCC	429
	TTA GGG GGC GTT GCC AGG GCC CTG GCG CAT GGC GTC CGG	468
	GTT CTG GAG GAC GGC GTG AAT TAC GCA ACA GGG AAT TTG	507
	CCT GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG CTG	546
35	TCC TGC TTG ACC ATC CCA GCT TCC GCT	573

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(2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

10	ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACC AAC CGT CGC CCA CAG GAC GTT AAG TTC CCG GGC	78
	GGC GGC CAG ATC GTT GGC GGA GTA TAC TTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACA AGG AAG ACT	156
	TCG GAG CGA TCC CAG CCA CGT GGG AGG CGC CAG CCC ATC	195
	CCC AAA GAT CGG CGC TCC ACT GGC AAG TCC TGG GGA AAA	234
	CCA GGA TAT CCC TGG CCC CTG TAT GGG AAT GAG GGA CTC	273
15	GGC TGG GCA GGA TGG CTC CTG TCC CCC CGA GGT TCC CGT	312
	CCC TCC TGG GGC CCC AAT GAC CCC CGG CAT AGG TCG CGC	351
	AAC GTG GGT AAG GTC ATC GAT ACC CTA ACG TGC AGC CTT	390
	GCC GAC CTC ATG GGG TAC GTC CCC GTC GTA GGC GGC CCG	429
	TTG GGT GGC GTC GCC AGA GCT CTC GCG CAT GGC GTG AGA	468
	GTC CTG GAG GAC GGG GTT AAT TAT GCA ACA GGG AAC TTA	507
	CCT GGT TGC TCC TTT TCT ATT TTC TTG CTG GCC CTA CTG	546
20	TCC TGC ATC ACC ATT CCA GTC TCC GCT	573

(2) INFORMATION FOR SEQ ID NO: 126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

30	ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACT AAC CGT CGC CCA CAA GAC GTT AAG TTT CCG GGC	78
	GGC GGC CAG ATC GTT GGC GGA GTA TAC TTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACA AGG AAG ACT	156
	TCG GAG CGG TCC CAG CCA CGT GGG AGG CGC CAG CCC ATC	195
	CCC AAA GAT CGG CGC CCC ACT GGC AAG TCC TGG GGA AAA	234
35	CCA GGA TAC CCT TGG CCC CTA TAT GGG AAT GAG GGA CTC	273

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GGC TGG GCA GGA TGG CTC CTG TCC CCC CGA GGT TCC CGT 312
 CCC TCT TGG GGC CCC ACT GAT CCC CGG CAT AGG TCG CGC 351
 AAC GTG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGC TTT 390
 GCC GAC CTC ATG GGA TAC ATC CCC GTC GTG GGC GCT CCG 429
 CTT GGT GGC GTC GCC AGA GCT CTC GCG CAT GGC GTG AGG 468
 GTC CTG GAG GAC GGG GTT AAT TAT GCA ACA GGG AAC TTA 507
 5 CCC GGT TGC TCC TTT TCT ATC TTC TTG CTG GCC TTA CTG 546
 TCC TGC ATC ACC ATT CCA GTC TCT GCT 573

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 10 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T9

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

ATG AGC ACA AAT CCA AAA CCC CAA AGA AAA ACC ATA AGA 39
 AAC ACC AAC CGT CGC CCA CAG GAC GTT AAG TTC CCG GGC 78
 GGC GGC CAG ATC GTT GGC GGA GTA TAC TTG TTG CCG CGC 117
 AGG GGC CCT AGG TTG GGT GTG CGC ACG ACA AGG AAG ACT 156
 TCG GAG CGG TCC CAG CCA CGT GGG AGG CGC CAG CCC ATC 195
 20 CCC AAA GAT CGG CGC TCC ACT GGC AAG TCC TGG GGA AAA 234
 CCA GGA TAC CCC TGG CCT CTA TAT GGG AAT GAG GGA CTC 273
 GGC TGG GCG GGA TGG CTC CTG TCC CCC CGA GGT TCC CGT 312
 CCC TCT TGG GGC CCC AGT GAC CCC CGG CAT AGG TCG CGC 351
 AAC GTG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGC TTT 390
 GCC GAC CTC ATG GGG TAC ATC CCC GTC GTA GGC GCC CCG 429
 CTT GGT GGC GTT GCC AGA GCT CTC GCG CAC GGC GTG AGA 468
 GTC CTG GAG GAC GGG GTT AAT TAT GCA ACA GGG AAC CTA 507
 25 CCT GGT TGC TCT TTT TCT ATC TTC TTG CTG GCC CTA CTG 546
 TCC TGC ATC ACC ACT CCG GCC TCT GCT 573

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T2

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

	ATG	AGC	ACA	ATT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACT	AAC	CGT	CGC	CCA	CAA	GAC	GTT	AAG	TTT	CCG	GGC	78
	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTA	TAC	TTG	CTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACA	AGG	AAG	ACT	156
5	TCG	GAG	CGG	TCC	CAG	CCT	CGT	GGA	AGG	CGC	CAG	CCC	ATC	195
	CCT	AAA	GAT	CGG	CGC	TCC	ACT	GGC	AAG	TCC	TGG	GGA	AAA	234
	CCA	GGA	TAC	CCC	TGG	CCC	CTG	TAT	GGG	AAT	GAG	GGG	CTC	273
	GGC	TGG	GCA	GGA	TGG	CTC	CTG	TCC	CCC	CGA	GGT	TCT	CGT	312
	CCC	TCT	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CAT	AGG	TCG	CGC	351
	AAT	GTG	GGT	AAA	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGC	TTT	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCC	GTC	GTA	GGC	GCC	CCG	429
	CTT	GGT	GGT	GTC	GCC	AGA	GCT	CTT	GCG	CAT	GGC	GTG	AGA	468
10	GTC	CTG	GAG	GAC	GGA	GTT	AAT	TAT	GCA	ACA	GGT	AAC	TTA	507
	CCC	GGT	TGC	TCC	TTT	TCT	ATC	TTC	TTG	CTA	GCC	CTG	CTG	546
	TCC	TGC	ATC	ACT	ATT	CCG	GTT	TCA	GCT					573

(2) INFORMATION FOR SEQ ID NO: 129:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

	ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACA	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	78
	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	CTG	CCG	CGC	117
	AGG	GGC	CCT	AGG	TTG	GGT	GTG	CGC	GCG	ACA	AGG	AAG	ACT	156
25	TCC	GAG	CGA	TCC	CAG	CCG	CGT	GGG	AGA	CGC	CAG	CCC	ATC	195
	CCG	AAA	GAT	CGG	CGC	TCC	ACC	GGC	AAG	TCC	TGG	GGA	AAA	234
	CCA	GGA	TAT	CCT	TGG	CCT	CTT	TAC	GGA	AAC	GAG	GGC	TGC	273
	GGT	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGG	TCT	CGT	312
	CCT	ACT	TGG	GGC	CCC	ACT	GAC	CCC	CGG	CAT	AGA	TCA	CGT	351
	AAT	TTG	GGC	AGA	GTC	ATC	GAT	ACC	ATT	ACA	TGT	GGT	TTT	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCT	GTC	GTT	GGC	GCC	CCG	429
30	GTC	GGA	GGC	GTC	GCC	AGA	GCT	CTG	GCA	CAT	GGT	GTT	AGG	468
	GTC	CTG	GAA	GAC	GGG	ATA	AAC	TAT	GCA	ACA	GGG	AAT	TTG	507
	CCT	GGT	TGC	TCT	TTT	TCT	ATC	TTC	TTG	CTT	GCT	CTT	CTG	546
	TCA	TGC	TTC	ACA	GTG	CCA	GTG	TCT	GCA					573

(2) INFORMATION FOR SEQ ID NO: 130:

35 (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

	ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACA	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	78
	GGC	GGT	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	CTG	CCG	CGC	117
10	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACA	AGG	AAG	ACT	156
	TCC	GAG	CGA	TCC	CAG	CCG	CGT	GGG	AGA	CGC	CAG	CCC	ATC	195
	CCG	AAA	GAT	CGG	CGC	TCC	ACC	GGC	AAG	TCC	TGG	GGA	AAG	234
	CCA	GGA	TAT	CCT	TGG	CCT	CTG	TAC	GGA	AAC	GAG	GGC	TGC	273
	GGC	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGG	TCT	CGT	312
	CCT	ACT	TGG	GGC	CCC	ACT	GAC	CCC	CGG	CAC	AGA	TCA	CGT	351
	AAC	TTG	GGC	AAG	GTC	ATC	GAT	ACC	ATT	ACG	TGT	GGT	TTT	390
15	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCT	GTC	GTT	GGC	GCC	CCG	429
	GTC	GGA	GGC	GTC	GCC	AGA	GCT	CTG	GCA	CAC	GGT	GTT	AGG	468
	GTC	CTG	GAA	GAC	GGG	ATA	AAT	TAC	GCA	ACA	GGG	AAT	CTG	507
	CCT	GGT	TGC	TCC	TTT	TCT	ATC	TTT	TTA	CTT	GCT	CTT	CTG	546
	TCG	TGC	GCC	ACG	GTG	CCG	GTG	TCT	GCA					573

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

	ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAT	ACA	AAC	CGC	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGT	78
	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	CTG	CCG	CGC	117
30	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	ACG	ACA	AGG	AAG	ACT	156
	TCC	GAG	CGA	TCC	CAG	CCG	CGT	GGG	AGA	CGC	CAG	CCC	ATC	195
	CCG	AAA	GAT	CGG	CGC	TCC	ACC	GGC	AAG	CCC	TGG	GGA	AAG	234
	CCA	GGA	TAT	CCT	TGG	CCC	CTG	TAT	GGA	AAC	GAG	GGC	TGC	273
	GGC	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGG	TCT	CAT	312
	CCT	AAT	TGG	GGC	CCC	ACT	GAC	CCC	CGG	CAT	AAA	TCA	CGC	351
	AAT	TTG	GGT	AAA	GTC	ATC	GAC	ACC	ATT	ACG	TGT	GGT	TTT	390
35	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCT	GTC	GTC	GGC	GCC	CCG	429

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GTC	GGA	GGC	GTC	GCC	AGA	GCT	CTG	GCA	CAC	GGT	GTT	AGA	468
GTC	CTG	GAA	GAC	GGG	ATA	AAT	TAC	GCA	ACA	GGG	AAT	CTG	507
CCT	GGT	TGC	TCT	TTT	TCT	ATC	TTC	TTA	CTT	GCT	CTT	CTG	546
TCA	TGC	TGC	ACA	GTG	CCA	GTG	TCT	GCG					573

5 (2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
AAT	ACA	AAC	CGC	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGT	78
GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	CTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACA	AGG	AAG	ACT	156
TCC	GAG	CGA	TCC	CAG	CCG	CGT	GGG	AGA	CGC	CAG	CCC	ATC	195
CCG	AAA	GAT	CGG	CGC	TCC	ACC	GGC	AAG	TCC	TGG	GGA	AAG	234
CCA	GGA	TAT	CCT	TGG	CCC	CTG	TAT	GGA	AAC	GAG	GGC	TGC	273
GGC	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGG	TCT	CAT	312
CCT	AAT	TGG	GGC	CCC	ACT	GAC	CCC	CGG	CAT	AGA	TCA	CGC	351
AAT	TTG	GGC	AAA	GTC	ATC	GAC	ACC	ATT	ACG	TGT	GGT	TTT	390
GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCT	GTC	GTT	GGC	GCC	CCG	429
GTC	GGA	GGC	GTC	GCC	AGA	GCT	CTG	GCA	CAC	GGT	GTT	AGA	468
GTC	CTG	GAA	GAC	GGG	ATA	AAT	TAC	GCA	ACA	GGG	AAT	CTG	507
CCT	GGT	TGC	TCT	TTT	TCT	ATC	TTC	TTA	CTT	GCT	CTT	CTG	546
TCG	TGC	TTC	ACA	GTG	CCA	GTG	TCT	GCG					573

25 (2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
AAC	ACA	AAC	CGC	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGT	78

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	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	CTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACA	AGG	AAG	TCT	156
	TCC	GAG	CGA	TCC	CAG	CCG	CGT	GGG	AGG	CGC	CAG	CCC	ATC	195
	CCG	AAA	GAT	CGG	CGC	TCC	ACC	GGC	AAG	TCC	TGG	GGA	AAA	234
	CCG	GGA	TAT	CCT	TGG	CCC	CTG	TAT	GGA	AAC	GAG	GGC	TGC	273
	GGC	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGG	TCT	CGT	312
	CCT	ACT	TGG	GGC	CCC	ACT	GAC	CCC	CGG	CAT	AGA	TCA	CGC	351
	AAT	TTG	GGC	AAA	GTC	ATC	GAC	ACC	ATT	ACG	TGT	GGT	TTT	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCT	GTC	GTT	GGC	GCC	CCG	429
	GTT	GGA	GGC	GTC	GCC	AGA	GCT	CTG	GCA	CAC	GGT	GTT	AGG	468
	GTC	CTG	GAA	GAC	GGG	ATA	AAT	TAC	GCA	ACA	GGG	AAT	TTG	507
	CCT	GGT	TGC	TCT	TTT	TCT	ATC	TTC	TTG	CTT	GCT	CTT	CTG	546
	TCG	TGC	TGC	ACA	GTG	CCA	GTG	TCT	GCG					573

(2) INFORMATION FOR SEQ ID NO: 134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: homosapiens
 - (C) INDIVIDUAL ISOLATE: S83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

	ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACT	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGC	CAG	ATC	GTT	GGC	GGA	GTA	TAC	TTG	CTG	CCG	CGC	117
	AGG	GGC	CCG	AGA	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAA	ACT	156
	TCC	GAA	CGG	TCC	CAG	CCA	CGT	GGG	AGG	CGC	CAG	CCC	ATC	195
	CCT	AAA	GAT	CGG	CGC	ACC	ACT	GGC	AAG	TCC	TGG	GGA	AGG	234
	CCA	GGA	TAC	CCT	TGG	CCC	CTG	TAT	GGG	AAT	GAG	GGC	CTC	273
	GGC	TGG	GCA	GGG	TGG	CTC	CTG	TCC	CCC	CGC	GGT	TCT	CGC	312
	CCT	TCA	TGG	GGC	CCC	ACC	GAC	CCC	CGG	CAT	AAA	TCG	CGC	351
	AAC	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGT	TTT	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATA	CCC	GTC	GTT	GGC	GCT	CCC	429
	GTT	GGC	GGC	GTT	GCC	AGA	GCC	CTC	GCC	CAT	GGG	GTG	AGG	468
	GTT	CTG	GAG	GAC	GGG	ATA	AAT	TAT	GCA	ACG	GGG	AAT	TTG	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTT	CTC	TTG	GCC	CTC	TTG	546
	TCT	TGC	ATC	TCT	GTG	CCA	GTT	TCC	GCC					573

(2) INFORMATION FOR SEQ ID NO: 135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

5	ATG AGC ACA CTT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACC ATC CGT CGC CCA CAG GAC GTT AAG TTC CCG GGT	78
	GGC GGA CAG ATC GTT GGT GGA GTA TAC GTG TTG CCG CGC	117
	AGG GGC CCA CGA TTG GGT GTG CGC GCG ACG CGT AAA ACT	156
	TCT GAA CGG TCG CAG CCT CGC GGA CGA CGA CAG CCT ATC	195
	CCC AAG GCG CGT CGG AGC GAA GGC CGG TCC TGG GCT CAG	234
	CCC GGG TAC CCT TGG CCC CTC TAT GGT AAC GAG GGC TGC	273
10	GGG TGG GCA GGA TGG CTC CTG TCC CCA CGC GGC TCC CGT	312
	CCA TCT TGG GGC CCA AAC GAC CCC CGG CGA CGG TCC CGC	351
	AAT TTG GGT AAA GTC ATC GAT ACC CTT ACG TGC GGA TTC	390
	GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCT CCC	429
	GTA GGA GGC GTC GCA AGA GCC CTC GCG CAT GGC GTG AGG	468
	GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAC TTG	507
	CCC GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC	546
15	TCT TGC TTA ATT CAT CCA GCA GCT AGT	573

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

25	ATG AGC ACA CTT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACC ATC CGT CGC CCA CAG GAC GTT AAG TTC CCG GGT	78
	GGC GGA CAG ATC GTT GGT GGA GTA TAC GTG TTG CCG CGC	117
	AGG GGC CCA CGA TTG GGT GTG CGC GCG ACG CGT AAA ACT	156
	TCT GAA CGG TCA CAG CCT CGC GGA CGA CGA CAG CCT ATC	195
	CCC AAG GCG CGT CGG AGC GAA GGC CGG TCC TGG GCT CAG	234
	CCC GGG TAC CCT TGG CCC CTC TAT GGT AAT GAG GGC TGC	273
30	GGG TGG GCA GGG TGG CTC CTG TCC CCA CGC GGC TCC CGT	312
	CCA TCT TGG GGC CCA AAC GAC CCC CGG CGG AGG TCC CGC	351
	AAT TTG GGT AAA GTC ATC GAT ACC CTT ACG TGC GGA TTC	390
	GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCT CCC	429
	GTA GGA GGC GTC GCA AGA GCC CTC GCG CAT GGC GTG AGG	468
	GCC CTT GAA GAC GGG ATA AAT TTT GCA ACA GGG AAC TTG	507
	CCC GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC	546
35	TCC TGC TTA GTT CAT CCT GCA GCT AGT	573

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(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

10	ATG AGC ACA CTT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACC ATC CGT CGC CCA CAG GAC ATC AAG TTC CCG GGT	78
	GGC GGA CAG ATC GTT GGT GGA GTA TAC GTG TTG CCG CGC	117
	AGG GGC CCA CGA TTG GGT GTG CGC GCG ACG CGT AAA ACT	156
	TCT GAA CGG TCA CAG CCT CGC GGA CGG CGA CAG CCT ATC	195
	CCC AAG GCG CGT CGG AGC GAA GGC CGA TCC TGG GCT CAG	234
15	CCC GGG TAC CCT TGG CCC CTC TAT GGT AAC GAG GGC TGC	273
	GGG TGG GCA GGG TGG CTC CTG TCC CCA CGC GGC TCC CGT	312
	CCA TCT TGG GGC CCA AAT GAC CCC CGG CGG AGG TCC CGC	351
	AAT TTG GGT AAA GTC ATC GAT ACC CTT ACG TGC GGC TTC	390
	GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCT CCC	429
	GTA GGA GGC GTC GCA AGA GCC CTC GCG CAT GGC GTG AGG	468
	GCC CTT GAA GAC GGG ATA AAT TTT GCA ACA GGG AAC TTG	507
20	CCC GGT TGC TCT TTT TCT ATC TTC CTT CTT GCC CTG TTC	546
	TCT TGC TTA ATT CAT CCA GCA GCT AGT	573

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

30	ATG AGC ACA CTT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACC ATC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGT	78
	GGC GGA CAG ATC GTT GGT GGA GTA TAC GTG TTG CCG CGC	117
	AGG GGC CCA CGA TTG GGT GTG CGC GCG ACG CGT AAA ACT	156
	TCT GAA CGG TCA CAG CCT CGC GGA CGG CGA CAG CCT ATC	195
35	CCC AAG GCG CGT CGG AGC GAA GGC CGG TCC TGG GCT CAG	234
	CCT GGG TAC CCT TGG CCC CTC TAT GGT AAC GAG GGC TGC	273

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GGG TGG GCA GGG TGG CTC CTG TCC CCA CGC GGC TCC CGT 312
 CCA TCT TGG GGC CCA AAC GAC CCC CGG CGG AGG TCC CGC 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTC ACG TGC GGA TTC 390
 GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCT CCT 429
 GTA GGG GGC GTC GCA AGA GCC CTC GCG CAT GGC GTG AGG 468
 GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAC TTG 507
 5 CCC GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC 546
 TCT TGC CTA ATT CAT CCA GCA GCT AGT 573

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 10 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z4

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
 AAC ACC AAC CGC CGC CCC ATG GAC GTA AAG TTC CCG GGT 78
 GGT GGC CAG ATC GTT GGC GGA GTT TAC TTG TTG CCG CGC 117
 AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT CGA AAG ACT 156
 TCG GAG CGG TCG CAA CCT CGT GGC AGG CGT CAA CCT ATC 195
 20 CCC AAG GCG CGC CAG CCA GAG GGC AGA TCC TGG GCG CAG 234
 CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TGC 273
 GGG TGG GCA GGG TGG CTC CTG TCT CCT CGC GGC TCT CGG 312
 CCA TCT TGG GGC CCA AAT GAT CCC CGG CGG AGA TCG CGC 351
 AAT CTG GGT AAG GTC ATC GAT ACC CTG ACG TGC GGC TTC 390
 GCC GAC CTC ATG GGA TAC ATC CCG ATC GTG GGC GCC CCC 429
 GTG GGG GGC GTC GCC AGG GCT CTG GCG CAT GGC GTC AGG 468
 25 GCT GTG GAG GAC GGG ATT AAC TAT GCA ACA GGG AAT CTT 507
 CCC GGT TGC TCT TTC TCT ATC TTC CTT TTG GCA CTT CTT 546
 TCG TGC CTC ACT GTT CCA GCG TCG GCT 573

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 35 (C) INDIVIDUAL ISOLATE: Z8

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGC	CGC	CCT	ATG	GAT	GTA	AAA	TTC	CCA	GGC	78
	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	CGG	AAG	ACT	156
5	TCG	GAG	CGG	TCG	CAA	CCT	CGT	GGC	AGG	CGT	CAG	CCT	ATC	195
	CCC	AAG	GCA	CGT	CGG	TCC	GAG	GGT	AGG	TCC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCA	TGG	CCT	CTT	TAC	GGT	AAT	GAA	GGC	TGT	273
	GGG	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGC	TCT	CGA	312
	CCG	TCT	TGG	GGC	CCA	AAT	GAT	CCC	CGG	CGG	AGG	TCG	CGC	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGC	TTC	390
	GCC	GAC	CTC	ATG	GGA	TAC	ATC	CCG	CTC	GTG	GGC	GCC	CCA	429
	GTA	GGA	GGC	GTC	GCC	AGA	GCC	CTG	GCG	CAT	GGC	GTC	AGG	468
10	GCT	GTG	GAG	GAC	GGG	ATC	AAC	TAT	GCA	ACA	GGG	AAC	CTT	507
	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCA	CTT	CTC	546
	TCG	TGC	CTA	ACC	GTC	CCA	GCG	TCT	GCT					573

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: Z1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

	ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGT	CGC	CCC	ATG	GAT	GTG	AAA	TTC	CCG	GGC	78
	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	CTG	CCG	CGC	117
	AGG	GGC	CCC	CGG	TTG	GGT	GTG	CGC	GCA	GCT	CGG	AAG	ACT	156
25	TCG	GAG	CGG	TCA	CAA	CCT	CGT	GGC	AGG	CGT	CAG	CCT	ATC	195
	CCC	AAG	GCG	CGC	CGG	TCC	GAG	GGC	AGG	TCC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTT	TAC	GGC	AAT	GAG	GGC	TGT	273
	GGG	TGG	GCA	GGG	TGG	CTC	CTG	TCC	CCC	CGC	GGT	TCC	AGG	312
	CCG	TCT	TGG	GGC	CCC	AAT	GAT	CCC	CGG	CGT	AGG	TCC	CGT	351
	AAT	CTG	GGT	AAA	GTC	ATC	GAT	ACC	CTG	ACG	TGT	GGC	TTC	390
	GCC	GAC	CTC	ATG	GGA	TAC	ATT	CCG	CTC	GTA	GGC	GCC	CCT	429
30	GTG	GGT	GGC	GTC	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	AGG	468
	GCC	GTG	GAG	GAC	GGA	ATT	AAC	TAC	GCA	ACA	GGG	AAC	CTT	507
	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTT	CTT	CTT	GCA	CTT	CTC	546
	TCG	TGC	CTG	ACA	ACA	CCA	GCA	TCT	GCC					573

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGC	CGC	CCC	ATG	GAT	GTA	AAA	TTC	CCG	GGT	78
	GGT	GGT	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	CGG	AAG	ACT	156
10	TCG	GAG	CGG	TCG	CAA	CCT	CGC	GGC	AGG	CGT	CAG	CCT	ATC	195
	CCC	CAG	GCA	CGT	CGG	TCC	GAG	GGC	AGG	TCC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCT	CTT	TAT	GGC	AAT	GAG	GGC	TGT	273
	GGG	TGG	GCA	GGG	TGG	CTC	CTG	TCC	CCC	CGC	GGA	TCT	CGG	312
	CCA	TCT	TGG	GGC	CAA	AAT	GAT	CCC	CGG	CGT	AGG	TCC	CGC	351
	AAT	CTG	GGT	AAG	GTC	ATC	GAT	ACC	CTG	ACG	TGT	GGC	TTC	390
	GCC	GAC	CTC	ATG	GGA	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCA	429
15	GTA	GGT	GGC	GTC	GCC	AGG	GCC	TTG	GCG	CAT	GGC	GTC	AGG	468
	GCC	CTG	GAG	GAC	GGA	ATC	AAC	TAT	GCA	ACA	GGG	AAT	CTT	507
	CCT	GGT	TGC	TCC	TTT	TCT	ATC	TTC	CTA	CTT	GCA	CTT	TTC	546
	TCG	TGC	TTG	ACA	ACA	CCG	GCA	TCC	GCT					573

(2) INFORMATION FOR SEQ ID NO: 143:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGC	CGC	CCC	ATG	GAC	GTT	AAG	TTC	CCG	GGT	78
	GGT	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	AGG	AAG	ACT	156
30	TCG	GAG	CGG	TCG	CAA	CCT	CGT	GGG	AGA	CGC	CAG	CCT	ATC	195
	CCC	AAG	GCA	CGT	CGA	TCT	GAG	GGA	AGG	TCC	TGG	GCT	CAG	234
	CCC	GGG	TAT	CCA	TGG	CCT	CTT	TAC	GGT	AAT	GAG	GGT	TGC	273
	GGG	TGG	GCG	GGA	TGG	CTC	CTG	TCA	CCC	CGT	GGC	TCT	CGA	312
	CCG	TCT	TGG	GGT	CCA	AAT	GAT	CCC	CGG	CGA	AGG	TCC	CGC	351
	AAC	TTG	GGT	AAG	GTC	ATC	GAT	ACT	CTA	ACT	TGC	GGT	TTC	390
	GCC	GAT	CTC	ATG	GGA	TAC	ATC	CCG	CTC	GTA	GGC	GCC	CCC	429
35	GTG	GGC	GGC	GTC	GCC	AGG	GCC	CTG	GCA	CAT	GGT	GTT	AGG	468

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GCT	GTG	GAG	GAC	GGG	ATC	AAT	TAT	GCA	ACA	GGG	AAT	CTT	507
CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCA	CTT	CTT	546
TCG	TGC	CTA	ACT	GTT	CCC	ACC	TCG	GCC					573

(2) INFORMATION FOR SEQ ID NO: 144:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCC	ATG	GAC	GTT	AAG	TTC	CCG	GGC	78
GGT	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
AGG	GGC	CCC	AGA	TTG	GGT	GTG	CGC	ACA	ACT	AGG	AAG	ACT	156
TCG	GAG	CGG	TCG	CAA	CCT	CGT	GGG	AGA	CGT	CAG	CCT	ATC	195
CCC	AAG	GCA	CGT	CGA	TCT	GAG	GGA	AGG	TCC	TGG	GCT	CAA	234
CCC	GGG	TAC	CCA	TGG	CCT	CTT	TAC	GGT	AAC	GAG	GGT	TGC	273
GGG	TGG	GCA	GGA	TGG	CTC	TTG	TCA	CCC	CGT	GGC	TCT	CGA	312
CCG	TCT	TGG	GGC	CCA	AAT	GAT	CCC	CGG	CGA	AGG	TCC	CGC	351
AAC	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACC	TGC	GGC	TTT	390
GCC	GAC	CTC	ATG	GGA	TAC	ATC	CCG	CTC	GTA	GGC	GCC	CCC	429
GTG	GGC	GGC	GTC	GCC	AGG	GCC	CTA	GCG	CAT	GGC	GTT	AGG	468
GCT	CTG	GAG	GAC	GGG	ATT	AAT	TAT	GCA	ACA	GGG	AAC	CTT	507
CCC	GGT	TGC	TCT	TTT	TCT	ATC	TTC	CTC	TTG	GCA	CTT	CTT	546
TCG	TGC	CTG	ACT	GTT	CCC	GCC	TCG	GCC					573

(2) INFORMATION FOR SEQ ID NO: 145:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCA	ATG	GAC	GTT	AAG	TTC	CCG	GGT	78
GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117

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AGG GGC CCT AGA TTG GGT GTG CGC GCG ACT AGG AAG ACT 156
 TCG GAG CGG TCG CAA CCT CGT GGG AGG CGC CAG CCT ATC 195
 CCC AAG GCG CGC CAA CTC GAG GGT AGG TCC TGG GCT CAG 234
 CCT GGG TAT CCT TGG CCC CTT TAC GGC AAT GAG GGC TGC 273
 GGG TGG GCG GGA TGG CTC CTG TCA CCC CGT GGC TCT CGG 312
 CCG TCT TGG GGC CCG AAT GAT CCC CGG CGG AGG TCC CGC 351
 AAC TTG GGT AAG GTC ATC GAT ACC CTA ACT TGC GGC TTC 390
 GCC GAC CTC ATG GGA TAC ATC CCG GTC GTA GGC GCC CCC 429
 GTG GGT GGC GTC GCC AGA GCC CTG GCG CAT GGC GTC AGG 468
 CTT CTG GAG GAC GGG GTC AAT TAT GCA ACA GGG AAT CTT 507
 CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCA CTG CTC 546
 TCG TGC CTG ACT GTT CCC GCT TCG GCC 573

10 (2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA 39
 AAC ACC AAC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGC 78
 GGT GGT CAG ATC GTT GGT GGA GTC TAC TTG TTG CCG CGC 117
 AGG GGC CCT AGG TTG GGT GTG CGC GCG ACT CGG AAG ACT 156
 TCA GAA CGG TCG CAA CCC CGT GGG CGG CGC CAG CCT ATT 195
 CCC AAG GCG CGC CAA CCC ACG GGC CGG TCC TGG GGT CAA 234
 CCC GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC 273
 GGG TGG GCA GGG TGG TTG CTC TCC CCC CGA GGC TCT CGG 312
 CCT AAT TGG GGC CCC AAT GAC CCC CGG CGA AAG TCG CGC 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC 390
 GCC GAC CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC 429
 GTT GGG GGC GTC GCA AGG GCC CTT GCA CAT GGT GTG AGG 468
 GTT CTT GAG GAC GGG GTA AAC TAT GCA ACG GGG AAT TTG 507
 CCC GGT TGC TCT TTC TCT ATC TTT ATC CTT GCA CTT CTC 546
 TCG TGC CTG ACC GTC CCG GCC TCT GCA 573

30 (2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

5	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC	117
	AGG GGC CCT AGA TTG GGT GTG CGC GCG ACT CGG AAG ACT	156
	TCA GAA CGG TCG CAA CCC CGT GGG CGG CGC CAG CCT ATT	195
	CCC AAG GCG CGC CAA CCC ACG GGC CGG TCC TGG GGT CAA	234
	CCC GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC	273
	GGG TGG GCA GGG TGG TTG CTC TCC CCC CGA GGC TCT CGG	312
10	CCT AAT TGG GGC CCC AAT GAC CCC CGG CGA AAA TCG CGC	351
	AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC	390
	GCC GAC CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC	429
	GTT GGG GGC GTC GCA AGG GCC CTC GCA CAT GGT GTG AGG	468
	GTT CTT GAG GAC GGG GTA AAC TAT GCA ACA GGG AAT TTG	507
	CCC GGT TGC TCT TTC TCT ATC TTT ATC CTT GCA CTT CTC	546
	TCG TGC TTG ACC GTC CCA GCC TCT GCA	573

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

25	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC	117
	AGG GGC CCT AGG TTG GGT GTG CGC GCG ACT CGG AAG ACT	156
	TCA GAA CGG TCG CAA CCC CGT GGG CGG CGC CAG CCT ATT	195
	CCC AAG GCG CGC CAA CCC ACG GGC CGG TCC TGG GGT CAA	234
	CCC GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC	273
	GGG TGG GCA GGG TGG TTG CTC TCC CCC CGA GGC TCT CGG	312
30	CCT AAT TGG GGC CCC AAT GAC CCC CGG CGA AAG TCG CGC	351
	AAT TTG GGT AAG GTC ATC GAC ACC CTA ACA TGC GGA TTC	390
	GCC GAC CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC	429
	GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG	468
	GTT CTT GAG GAC GGG GTA AAT TAC GCA ACA GGG AAT CTG	507
	CCC GGT TGC TCT TTC TCT ATC TTT ATC CTT GCA CTT CTC	546
	TCG TGC CTG ACC GTC CCA GCC TCC GCA	573

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(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

10	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACC AAC CTC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT CGG AAG ACT	156
	TCG GAA CGG TCG CAA CCC CGT GGG CGG CGC CAG CCT ATT	195
	CCC AAG GCG CGC CAA CCC ACG GGC CGG TCC TGG GGT CAA	234
	CCC GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC	273
15	GGG TGG GCA GGG TGG TTG CTC TCC CCC CGA GGC TCT CGG	312
	CCT AAT TGG GGC CCC AAT GAC CCC CGG CGG AAG TCG CGC	351
	AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC	390
	GCC GAC CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC	429
	GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG	468
	GTT CTT GAG GAC GGG GTA AAC TAC GCA ACA GGG AAT TTG	507
	CCC GGT TGC TCT TTC TCT ATC TTT ATC CTT GCA CTT CTT	546
20	TCC TGT CTG ATC ATC CCG GCC TCT GCA	573

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

30	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT CGG AAG ACT	156
	TCA GAA CGG TCG CAA CCC CGT GGA CGG CGC CAG CCT ATT	195
	CCC AAG GCT CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA	234
	CCC GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC	273
35	GAG TGG GCA GGG TGG TTG CTC TCC CCC CGA GGC TCT CGG	312

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CCT AGT TGG GGC CCC AAC GAC CCC CGG CGG AAA TCG CGC 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC 390
 GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC 429
 GTT GGG GGC GTC GCA AGG GCT CTC GCA CAT GGT GTG AGG 468
 GTT CTT GAG GAC GGG GTA AAC TAC GCA ACA GGG AAT TTA 507
 CCC GGT TGC TCT TTC TCT ATC TTT ATC CTT GCA CTT CTT 546
 TCA TGC CTG ACC GTC CCG GCC TCT GCA 573

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA 39
 AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC 78
 GGT GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC 117
 AGG GGC CCT AGG TTG GGT GTG CGC GCA ACT CGG AAG ACT 156
 TCA GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG CCT ATC 195
 CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA 234
 CCC GGG TAC CCT TGG CCC CTT TAT GCC AAT GAG GGC CTC 273
 GGG TGG GCA GGG TGG TTG CTC TCC CCC CGA GGC TCT CGG 312
 CCT AAT TGG GGC CCC AAT GAC CCC CGG CGG AAA TCG CGC 351
 AAC TTG GGT AAG GTC ATC GAT ACC CTG ACG TGC GGA TTC 390
 GCC GAC CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC 429
 GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG 468
 GTC CTT GAG GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA 507
 CCC GGT TGC TCT TTC TCT ATC TTT ATC CTT GCA CTT CTT 546
 TCA TGC CTG ACT GTC CCG ACC TCT GCC 573

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA6

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	CAA	AGA	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCT	CGT	ATG	GGT	GTG	CGC	GCG	ACT	CGG	AAG	ACT	156
5	TCG	GAA	CGG	TCG	CAA	CCC	CGT	GGA	CGG	CGT	CAG	CCT	ATT	195
	CCC	AAG	GCG	CGC	CAA	TCC	GCG	GGT	CGG	TCC	TGG	GGT	CAA	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTT	TAC	GCC	AAT	GAG	GGC	CTC	273
	GGG	TGG	GCA	GGG	TGG	TTG	CTC	TCC	CCC	CGA	GGC	TCT	CGG	312
	CCT	AAT	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CGA	AAA	TCG	CGC	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGA	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTA	GGC	GGC	CCC	429
10	GTT	GGG	GGC	GTC	GCA	AGG	GCT	CTC	GCA	CAC	GGT	GTG	AGG	468
	GTT	CTT	GAG	GAC	GGG	GTA	AAC	TAT	GCA	ACA	GGG	AAT	TTG	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTT	GTC	CTT	GCA	CTT	CTC	546
	TCG	TGC	CTA	ACC	GTC	CCT	GCC	TCT	GCA					573

(2) INFORMATION FOR SEQ ID NO: 153:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA11

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
25	AGG	GGC	CCT	AGG	TTG	GGT	GTG	CGC	GCG	ACT	CGG	AAG	ACT	156
	TCA	GAA	CGG	TCG	CAA	CCC	CGT	GGG	CGG	CGT	CAG	CCT	ATT	195
	CCC	AAG	GCG	CGC	CAA	CCC	ACG	GGC	CGG	TCC	TGG	GGT	CAA	234
	CCC	GGG	TAC	CCT	TGG	CCC	TTT	TAC	GCC	AAT	GAG	GGC	CTC	273
	GGG	TGG	GCA	GGG	TGG	CTG	CTC	TCC	CCT	CGA	GGC	TCT	CGG	312
	CCT	AAC	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CGA	AGA	TCG	CGC	351
	AAT	TTG	GGC	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGA	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTA	GGC	GGC	CCC	429
30	GTT	GGG	GGC	GTC	GCA	AGG	GCC	CTC	GCA	CAC	GGT	GTG	AGA	468
	GCT	CTT	GAG	GAC	GGG	GTA	AAT	TAT	GCA	ACA	GGG	AAT	CTT	507
	CCC	GGT	TGC	TCT	TTC	TCC	ATC	TTT	ATC	CTT	GCA	CTT	CTC	546
	TCG	TGC	TTG	ACC	GTC	CCG	GCC	ACT	GCA					573

(2) INFORMATION FOR SEQ ID NO: 154:

35 (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

	ATG	AGC	ACA	CTT	CCA	AAA	CCC	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACC	AAC	CGT	CGC	CCA	ACG	GAC	GTC	AAG	TTC	CCG	GGT	78
	GGC	GGT	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
10	AGG	GGC	CCC	CGG	TTG	GGT	GTG	CGC	GCG	ACG	AGA	AAG	ACT	156
	TCC	GAG	CGA	TCC	CAG	CCC	AGA	GGC	AGG	CGC	CAA	CCT	ATA	195
	CCA	AAG	GCG	CGC	CAG	CCC	CAG	GGC	AGG	CAC	TGG	GCT	CAG	234
	CCC	GGA	TAC	CCT	TGG	CCT	CTT	TAT	GGA	AAC	GAG	GGC	TGT	273
	GGG	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGC	TCC	CGG	312
	CCA	CAT	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CGT	CGA	TCC	CGG	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGT	GGG	TTC	390
	GCC	GAT	CTC	ATG	GGG	TAC	ATT	CCC	GTC	GTG	GGC	GCG	CCT	429
15	TTG	GGC	GGC	GTC	GCG	GCT	GCG	CTC	GCA	CAT	GGC	GTG	AGG	468
	GCA	ATC	GAG	GAC	GGG	ATC	AAT	TAT	GCA	ACA	GGG	AAT	CTC	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	TTG	GCA	CTA	CTC	546
	TCG	TGC	CTC	ACA	ACG	CCA	GCT	TCG	GCT					573

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
30	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30				35					40				
	Arg	Leu	Gly	Val	Arg	Ala	Pro	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45				50					55				
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
	60				65					70				

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°	Pro	Glu	Gly	Arg	Thr	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
					75					80				
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85					90					95			
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
	100						105					110		
	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
			115					120					125	
5	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
				130					135					140
	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly
					145					150				
	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
	155					160					165			
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
		170					175							
10	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala					
			185					190						

(2) INFORMATION FOR SEQ ID NO: 156:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
25	15					20					25			
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
		30					35					40		
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
			45					50					55	
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
				60					65					70
	Pro	Glu	Gly	Arg	Thr	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
30					75					80				
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85					90					95			
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
		100					105					110		
	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
			115					120					125	
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
35				130					135					140

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Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 5 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

15 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 20 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 25 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 30 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190
 35

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(2) INFORMATION FOR SEQ ID NO: 158:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

5	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20				25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
		30					35				40			
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
			45					50					55	
10	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
				60					65					70
	Pro	Glu	Gly	Arg	Thr	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
					75					80				
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85					90					95			
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
		100					105					110		
15	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
			115					120					125	
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
				130					135					140
	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly
					145					150				
	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
20						160					165			
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
		170					175					180		
	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala					
			185					190						

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DR4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

35	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				

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0 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 5 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 10 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 15 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 161:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 25 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:
 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 30 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 35 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80

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Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 5 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Pro Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 10 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Met Ser Thr Asn Pro Lys Pro Gln Arg Ala Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 25 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly His Pro Trp Pro
 75 80
 30 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 35

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° Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

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(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: D1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

15

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

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(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

10	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30				35					40				
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45				50					55				
15	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
	60				65					70				
	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
	75				80					85				
	Leu	Tyr	Gly	Asn	Glu	Gly	Met	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85				90					95				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
	100				105					110				
20	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
	115				120					125				
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
	130				135					140				
	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly
	145				150					155				
25	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
	155				160					165				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
	170				175					180				
	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala					
	185				190									

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: P10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

5	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20					25			
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Gly	Gly	Pro
		30					35					40		
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
			45					50					55	
10	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
				60					65					70
	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
					75					80				
	Leu	Tyr	Gly	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85					90					95			
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
		100					105					110		
15	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
			115					120					125	
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
				130					135					140
	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly
					145					150				
	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
20	155					160					165			
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
		170					175					180		
	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala					
			185					190						

25 (2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

30 (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

35	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				

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° Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 5 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 10 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 15 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 167:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 25 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 30 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 35 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80

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Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 5 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 10 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 25 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 30 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 35

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° Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

5

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

15

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

35

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(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

10	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30				35					40				
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45				50					55				
15	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
	60				65					70				
	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly	His	Pro	Trp	Pro
	75				80					85				
	Leu	Tyr	Gly	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	90				95					100				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
20	105				110					115				
	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
	120				125					130				
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
	135				140					145				
	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly
	150				155					160				
25	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
	165				170					175				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
	180				185					190				
	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala					

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
5	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20				25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
		30				35					40			
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
			45					50					55	
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	His
10				60					65					70
	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
					75					80				
	Leu	Tyr	Gly	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	Leu	Leu
		85				90					95			
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro
		100					105					110		
15	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
								120					125	
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
				130					135					140
	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly
					145					150				
	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
	155					160					165			
20	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
		170					175					180		
	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala					
			185					190						

(2) INFORMATION FOR SEQ ID NO: 172:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

30 (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
35	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20					25			

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Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 5 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 10 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 15 Ser Cys Leu Thr Thr Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 25 (C) INDIVIDUAL ISOLATE: HK5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:
 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 30 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 35

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0 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro His Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 5 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Ile Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 10 Ser Cys Leu Thr Thr Pro Val Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK4

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 25 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 30 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 35 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150

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Val Arg Val Val Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

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(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: P8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

15 Met Ser Thr Thr Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Ser Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 20 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly His Pro Trp Pro
 75 80
 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 25 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 30 Val Arg Val Val Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

35

(2) INFORMATION FOR SEQ ID NO: 176:

SUBSTITUTE SHEET (RULE 26)

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

5

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T3

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

10	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
		30				35					40			
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
		45				50						55		
15	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
			60				65					70		
	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
			75				80							
	Leu	Tyr	Gly	Asp	Glu	Gly	Met	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85				90					95				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Asn	Trp	Gly	Pro	Thr	Asp	Pro
		100				105					110			
20	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
			115				120					125		
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
			130					135					140	
	Gly	Ala	Pro	Leu	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
				145				150						
	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
	155				160					165				
25	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
		170				175						180		
	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala					
			185				190							

- (2) INFORMATION FOR SEQ ID NO: 177:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

35

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens

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(C) INDIVIDUAL ISOLATE: T4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
5	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
		30				35					40			
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
		45				50						55		
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Asp	Arg	Arg
		60				65						70		
10	Ser	Thr	Gly	Lys	Ser	Trp	Gly	Lys	Pro	Gly	Tyr	Pro	Trp	Pro
		75				80								
	Leu	Tyr	Gly	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85				90					95				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro
		100				105					110			
	Arg	His	Arg	Ser	Arg	Asn	Val	Gly	Lys	Val	Ile	Asp	Thr	Leu
		115				120						125		
15	Thr	Cys	Ser	Leu	Ala	Asp	Leu	Met	Gly	Tyr	Val	Pro	Val	Val
		130				135							140	
	Gly	Gly	Pro	Leu	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
		145				150								
	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
	155				160					165				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
		170				175					180			
20	Ser	Cys	Ile	Thr	Ile	Pro	Val	Ser	Ala					
		185				190								

(2) INFORMATION FOR SEQ ID NO: 178:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US10

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
35	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				

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° Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 5 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 10 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 15 Ser Cys Ile Thr Ile Pro Val Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- 25 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

30 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Ile Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 30 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Thr Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80

35

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° Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Ser Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 5 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 10 Ser Cys Ile Thr Thr Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T2

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Met Ser Thr Ile Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 25 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 30 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 35 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150

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Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Ile Thr Ile Pro Val Ser Ala
 185 190

5

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

15 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 20 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 25 Ser Pro Arg Gly Ser Arg Pro Thr Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Leu Gly Arg Val Ile Asp Thr Ile
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 30 Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Phe Thr Val Pro Val Ser Ala
 185 190

35

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(2) INFORMATION FOR SEQ ID NO: 182:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

5

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

10	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20					25			
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
		30					35					40		
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
		45					50					55		
15	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Asp	Arg	Arg
		60					65					70		
	Ser	Thr	Gly	Lys	Ser	Trp	Gly	Lys	Pro	Gly	Tyr	Pro	Trp	Pro
				75						80				
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85				90					95				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Thr	Trp	Gly	Pro	Thr	Asp	Pro
	100					105					110			
20	Arg	His	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Ile
		115					120					125		
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Val	Val
			130					135					140	
	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
				145				150						
	Val	Arg	Val	Leu	Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn
	155				160				165					
25	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
	170				175						180			
	Ser	Cys	Ala	Thr	Val	Pro	Val	Ser	Ala					
		185					190							

(2) INFORMATION FOR SEQ ID NO: 183:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

35

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens

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(C) INDIVIDUAL ISOLATE: DK11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
5	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20				25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
		30					35				40			
	Arg	Leu	Gly	Val	Arg	Thr	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
			45					50				55		
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Asp	Arg	Arg
				60					65				70	
10	Ser	Thr	Gly	Lys	Pro	Trp	Gly	Lys	Pro	Gly	Tyr	Pro	Trp	Pro
					75					80				
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85					90				95				
	Ser	Pro	Arg	Gly	Ser	His	Pro	Asn	Trp	Gly	Pro	Thr	Asp	Pro
		100					105				110			
	Arg	His	Lys	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Ile
			115					120				125		
15	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Val	Val
				130					135				140	
	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
					145				150					
	Val	Arg	Val	Leu	Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn
	155					160				165				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
		170					175				180			
20	Ser	Cys	Cys	Thr	Val	Pro	Val	Ser	Ala					
			185					190						

(2) INFORMATION FOR SEQ ID NO: 184:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
35	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20				25				

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° Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 5 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser His Pro Asn Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Ile
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 10 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 15 Ser Cys Phe Thr Val Pro Val Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Ser Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 35 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95

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Ser Pro Arg Gly Ser Arg Pro Thr Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Ile
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 5 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Cys Thr Val Pro Val Ser Ala
 185 190

10

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

20

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 25 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Thr Thr Gly Lys Ser Trp Gly Arg Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 30 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 35 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150

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Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Ile Ser Val Pro Val Ser Ala
 185 190

5

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

10

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: HK10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

15 Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Ile Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Val Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 20 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 25 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 30 Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
 170 175 180
 Ser Cys Leu Ile His Pro Ala Ala Ser
 185 190

35

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° (2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

10	Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Ile	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Val	Leu	Pro	Arg	Arg	Gly	Pro
		30				35					40			
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
		45				50					55			
15	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
		60				65					70			
	Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
		75				80								
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85				90					95				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro
	100				105						110			
20	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
		115				120					125			
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
		130				135								
	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
		145				150								
	Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	Gly	Asn
	155				160					165				
25	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe
	170				175							180		
	Ser	Cys	Leu	Val	His	Pro	Ala	Ala	Ser					
		185				190								

(2) INFORMATION FOR SEQ ID NO: 189:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens

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(C) INDIVIDUAL ISOLATE: S2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

	Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
5	Thr	Ile	Arg	Arg	Pro	Gln	Asp	Ile	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Val	Leu	Pro	Arg	Arg	Gly	Pro
		30				35					40			
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
		45					50					55		
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
		60						65					70	
10	Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
		75						80						
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85				90					95				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro
	100					105					110			
	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
		115					120					125		
15	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
		130						135					140	
	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
			145					150						
	Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	Gly	Asn
	155				160					165				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe
20		170				175					180			
	Ser	Cys	Leu	Ile	His	Pro	Ala	Ala	Ser					
		185					190							

(2) INFORMATION FOR SEQ ID NO: 190:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

	Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Ile	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
35	15				20					25				

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° Gln Ile Val Gly Gly Val Tyr Val Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 5 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 10 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
 170 175 180
 15 Ser Cys Leu Ile His Pro Ala Ala Ser
 185 190

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z4

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 30 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 35 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95

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Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Ile Val
 130 135 140
 5 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

10

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

20

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 25 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 30 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150

35

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° Val Arg Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

5 (2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

15 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Ala Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 20 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 25 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 30 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Thr Pro Ala Ser Ala
 185 190

35 (2) INFORMATION FOR SEQ ID NO: 194:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
10	Thr	Asn	Arg	Arg	Pro	Met	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20					25			
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
		30					35					40		
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
			45					50					55	
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Gln	Ala	Arg	Arg
				60					65					70
15	Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
					75					80				
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85					90				95				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Gln	Asn	Asp	Pro
		100					105					110		
	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
20								120					125	
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
				130					135					140
	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
					145					150				
	Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn
	155					160				165				
25	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe
		170					175					180		
	Ser	Cys	Leu	Thr	Thr	Pro	Ala	Ser	Ala					
			185					190						

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z6

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 5 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 10 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 15 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 20 Ser Cys Leu Thr Val Pro Thr Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 35 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40

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Arg Leu Gly Val Arg Thr Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 5 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 10 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190
 15

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 20 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

25 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 30 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Leu Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 35 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95

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° Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 5 Val Arg Leu Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

10

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

20 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 25 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 30 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 35 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165

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Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

5 (2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 15 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 20 Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 25 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 30 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 200:

35 (i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
10	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
		30				35						40		
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
		45						50					55	
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Gln
			60						65				70	
	Pro	Thr	Gly	Arg	Ser	Trp	Gly	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
15					75					80				
	Leu	Tyr	Ala	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85					90				95				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Asn	Trp	Gly	Pro	Asn	Asp	Pro
		100					105					110		
	Arg	Arg	Lys	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
			115					120					125	
20	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
				130					135					140
	Gly	Gly	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
					145					150				
	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
	155					160					165			
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Ile	Leu	Ala	Leu	Leu
		170					175					180		
25	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala					
			185					190						

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA1

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Leu Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 5 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 10 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 15 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Ile Ile Pro Ala Ser Ala
 185 190
 20

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 35 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40

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° Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Ala Asn Glu Gly Leu Glu Trp Ala Gly Trp Leu Leu
 85 90 95
 5 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 10 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

15

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

20

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA13

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

25 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 30 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110

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Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 5 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Thr Ser Ala
 185 190

10 (2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

20 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Gln Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Met Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 25 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Ser Ala Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 30 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 35 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165

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Leu Pro Gly Cys Ser Phe Ser Ile Phe Val Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

5 (2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 15 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 20 Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Phe Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 25 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 30 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Thr Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 206:

35 (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
1				5					10				
Thr	Asn	Arg	Arg	Pro	Thr	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
15					20					25			
Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30				35					40			
Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45				50					55			
Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Gln
	60				65					70			
Pro	Gln	Gly	Arg	His	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
	75				80					85			
Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
85				90					95				
Ser	Pro	Arg	Gly	Ser	Arg	Pro	His	Trp	Gly	Pro	Asn	Asp	Pro
100				105					110				
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
	115				120					125			
Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Val	Val
20			130					135					140
Gly	Ala	Pro	Leu	Gly	Gly	Val	Ala	Ala	Ala	Leu	Ala	His	Gly
			145					150					
Val	Arg	Ala	Ile	Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn
155				160					165				
Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
	170			175					180				
25	Ser	Cys	Leu	Thr	Thr	Pro	Ala	Ser	Ala				
			185					190					

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GCGTCCGGGT TCTGGAAGAC GCGTGAACT ATGCAACAGG

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(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGCTTTCAT TGCAGTTCAA GGCCGTGCTA TTGATGTGCC

40

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

AAGACGGCGT GAACTATGCA ACAGGGAACC TTCCTGGTTG

40

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

AGTTCAAGGC CGTGCTATTG ATGTGCCAAC TGCCGTTGGT

40

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

AAGACGGCGT GAATTCTGCA ACAGGGAACC TTCCTGGTTG

40

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(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

AGTTCAAGGC CGTGGGAATTC ATGTGCCAAC TGCCGTTGGT

40

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ARCTYCGACG TYACATCGAY CTGCTYGTYG GRAGYGCCAC CC

42

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

RCARGCCRTC TTGGAYATGA TCGCTGGWGC Y

31

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

CRATACGACR YCAYGTCGAY TTGCTCGTTG GGGCGGCTRY YT

42

(2) INFORMATION FOR SEQ ID NO:216:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:
RCAAGCTRTC RTGGAYRTGG TRRCRGGRGC C 31
- (2) INFORMATION FOR SEQ ID NO:217:
- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:
15 TTGCGGACKC ACATYGACAT GGTyGTGATG TCCGCCACGC 40
- (2) INFORMATION FOR SEQ ID NO:218:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:
GATGCGCGTT CCCGAGGTCA TCWTAGACAT CRTYRGCGR GCD 43
- 25 (2) INFORMATION FOR SEQ ID NO:219:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:
AATGGCACCY TGCRCCTGCTG GATACAAGTR ACACCTAATG TGGCTGTGAA 50
ACAC 54
- 35 (2) INFORMATION FOR SEQ ID NO:220:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:
TGARCTAGYC CTYSARGTYG TCTTCGGYGG Y 31
- (2) INFORMATION FOR SEQ ID NO:221:
- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:
15 GCCAACGTCT CTCGATGTTG GGTGCCGGTT GCCCCCAATC TCGCCATAAG 50
TCAA 54
- (2) INFORMATION FOR SEQ ID NO:222:
- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:
25 AAGGGCCTGC GAGCACACAT CGATATCATC GTGATGTCTG CTACGG 46
- (2) INFORMATION FOR SEQ ID NO:223:
- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:
TTGGTGCGCA TCCCGGAAGT CATCTTGAT ATTGTTACAG GAGGT 45
- 35 (2) INFORMATION FOR SEQ ID NO:224:

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o s

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

AGTCAGGTAY GTCGGAGCAA CCACCGCYTC GATACGCAGT

40

- (2) INFORMATION FOR SEQ ID NO:225:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

15

AGCCTTCACG TTCAGACCKC GTCGCCATCA AACRGTCAG ACCTGT

46

- (2) INFORMATION FOR SEQ ID NO:226:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

25

TCCCCGCGYG TGGGTATGGT GGTRGCGCAC RTYCTGCGDY TGCCCCAGAC
CKTGTTYGAC ATAMTRGCGY GGGCC

50
75

- (2) INFORMATION FOR SEQ ID NO:227:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

ACGCCGGTGA CGCCTACAGT GGCTGTCGCA CACCCGGGC

39

35

- (2) INFORMATION FOR SEQ ID NO:228:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:
ATGAGGGTCC CCACAGCCTT TCTCGACATG GTTGCCGGAG GC 42
- (2) INFORMATION FOR SEQ ID NO:229:
- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:
15 CGCGCCCTAT CCCAACGCAC CGTTAGAGTC CATGCGCAGG 40
- (2) INFORMATION FOR SEQ ID NO:230:
- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:
25 TCAGATCTTA CGGATCCCCT CTATCCTAGG TGA CTGCTC ACCGGGGGT 49
- (2) INFORMATION FOR SEQ ID NO:231:
- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:
35 CAGTCACGCT GCTGGGTGGC CCTTACTCCC ACCGTGGCGG YGYCTTATAT 50
CGGT 54

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° (2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

TAGCACTCTG GTRGAYCTAC TCRCTGGAGG G

31

(2) INFORMATION FOR SEQ ID NO:233:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

15 AAGTCTACAT GCTGGGTGTC TCTACCCCC ACCGTGGCTG CGCAACATCT
 GAAT

50
54

(2) INFORMATION FOR SEQ ID NO:234:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

25 AGGCGCCATG GTCGACCTGC TTGCAGGCGG C

31

(2) INFORMATION FOR SEQ ID NO:235:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

TCAGCCCCGA VYYTCGGAGC GGTCACGGCT CCTCTTCGGA GGG

43

35

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° (2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

TGYTACGGAT YCCCCARGTG GTCATHGACA TCATWGCCGG GGSC

44

(2) INFORMATION FOR SEQ ID NO:237:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

15

CATACCAAAT GCTTCCACGC CCGCAACGGG ATTCCGCAGG

40

(2) INFORMATION FOR SEQ ID NO:238:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

TCTTCTTGCG GCGCCGCAG TGGTTTGCTC ATCCCTG

37

25

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

ATCTAGCATC TTGAGGGTAC CTGAGATTG TGCGAGTGTG ATATTTGGTG
 GC

50

52

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(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Trp	Ile	Gln	Val	Thr	Pro	Asn	Val	Ala	Val	Lys	His	Arg	Gly	Ala
				5					10					15
Leu	Thr	His	Asn	Leu	Arg	Xaa	His	Xaa	Asp	Xaa	Ile	Val	Met	Ala
				20					25					30
Ala	Thr	Val												

10 (2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Trp	Val	Pro	Val	Ala	Pro	Asn	Leu	Ala	Ile	Ser	Gln	Pro	Gly	Ala
				5					10					15
Leu	Thr	Lys	Gly	Leu	Arg	Ala	His	Ile	Asp	Ile	Ile	Val	Met	Ser
				20					25					30
Ala	Thr	Val												

20 (2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Trp	Ile	Pro	Val	Xaa	Pro	Asn	Val	Ala	Val	Xaa	Xaa	Pro	Gly	Ala
				5					10					15
Leu	Thr	Gln	Gly	Leu	Arg	Thr	His	Ile	Asp	Met	Val	Val	Met	Ser
				20					25					30
Ala	Thr	Leu												

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids

35

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- (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

5 Trp Thr Xaa Val Thr Pro Thr Val Ala Val Arg Tyr Val Gly Ala
 5 10 15
 Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly Ala
 20 25 30
 Ala Thr Xaa

(2) INFORMATION FOR SEQ ID NO:244:

10

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

15

Trp Val Ala Leu Xaa Pro Thr Leu Ala Ala Arg Asn Xaa Xaa Xaa
 5 10 15
 Xaa Thr Xaa Xaa Ile Arg Xaa His Val Asp Leu Leu Val Gly Ala
 20 25 30
 Ala Xaa Phe

20

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Trp Val Xaa Xaa Xaa Pro Thr Val Ala Thr Arg Asp Gly Lys Leu
 5 10 15
 Pro Xaa Xaa Gln Leu Arg Arg Xaa Ile Asp Leu Leu Val Gly Ser
 20 25 30
 Ala Thr Leu

30

(2) INFORMATION FOR SEQ ID NO:246:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Trp Thr Pro Val Thr Pro Thr Val Ala Val Ala His Pro Gly Ala
 5 10 15
 Pro Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala
 5 20 25 30
 Ala Thr Leu

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Trp Val Ala Leu Thr Pro Thr Val Ala Xaa Xaa Tyr Ile Gly Ala
 5 10 15
 15 Pro Leu Xaa Ser Xaa Arg Arg His Val Asp Leu Met Val Gly Ala
 20 25 30
 Ala Thr Val

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

25 Trp Val Ser Leu Thr Pro Thr Val Ala Ala Gln His Leu Asn Ala
 5 10 15
 Pro Leu Glu Ser Leu Arg Arg His Val Asp Leu Met Val Gly Gly
 20 25 30
 Ala Thr Leu

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

35

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° (xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Pro Asn Ala
 5 10 15
 Pro Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala
 20 25 30
 Ala Thr Met

5

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Trp Val Xaa Ile Thr Pro Thr Leu Ser Ala Pro Xaa Xaa Gly Ala
 5 10 15
 Val Thr Ala Pro Leu Arg Arg Xaa Val Asp Tyr Leu Ala Gly Gly
 20 25 30
 Ala Ala Leu

15

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Trp His Ala Val Thr Pro Thr Leu Ala Ile Pro Asn Ala Ser Thr
 5 10 15
 Pro Ala Thr Gly Phe Arg Arg His Val Asp Leu Leu Ala Gly Ala
 20 25 30
 Ala Val Val

25

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

30

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° (xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro Glu Leu
 5 10 15
 Xaa Leu Xaa Val Val Phe Gly Gly
 20

5 (2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Thr Thr Thr Met Leu Leu Ala Tyr Leu Val Arg Ile Pro Glu Val
 5 10 15
 Ile Leu Asp Ile Val Thr Gly Gly
 20

15 (2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Thr Xaa Thr Xaa Ile Leu Ala Tyr Xaa Met Arg Val Pro Glu Val
 5 10 15
 Ile Xaa Asp Ile Xaa Xaa Gly Ala
 20

25 (2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Ala Val Gly Met Val Val Ala His Xaa Leu Arg Leu Pro Gln Thr
 5 10 15
 Xaa Phe Asp Ile Xaa Ala Gly Ala
 20

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(2) INFORMATION FOR SEQ ID NO:256:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Thr Xaa Ala Leu Val Xaa Ser Gln Leu Leu Arg Xaa Pro Gln Ala
 5 10 15
 Xaa Xaa Asp Xaa Val Xaa Gly Ala
 20

(2) INFORMATION FOR SEQ ID NO:257:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Thr Xaa Ala Leu Val Xaa Ala Gln Leu Leu Arg Xaa Pro Gln Ala
 5 10 15
 Xaa Leu Asp Met Ile Ala Gly Ala
 20

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Thr Thr Thr Leu Leu Leu Ala Gln Ile Met Arg Val Pro Thr Ala
 5 10 15
 Phe Leu Asp Met Val Ala Gly Gly
 20

(2) INFORMATION FOR SEQ ID NO:259:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid

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(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Thr Thr Thr Leu Xaa Leu Ala Gln Val Met Arg Ile Pro Ser Thr
 5 10 15
 5 Leu Val Asp Leu Leu Xaa Gly Gly
 20

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
 10 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Thr Ala Thr Leu Val Leu Ala Gln Leu Met Arg Ile Pro Gly Ala
 5 10 15
 15 Met Val Asp Leu Leu Ala Gly Gly
 20

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
 20 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Thr Ser Ala Leu Ile Met Ala Gln Ile Leu Arg Ile Pro Ser Ile
 5 10 15
 25 Leu Gly Asp Leu Leu Thr Gly Gly
 20

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
 30 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

35

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° Xaa Thr Ala Leu Xaa Met Ala Gln Xaa Leu Arg Ile Pro Gln Val
 5 10 15
 Val Ile Asp Ile Ile Ala Gly Xaa
 20

(2) INFORMATION FOR SEQ ID NO:263:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:
 10 Thr Thr Thr Leu Val Leu Ser Ser Ile Leu Arg Val Pro Glu Ile
 5 10 15
 Cys Ala Ser Val Ile Phe Gly Gly
 20

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CLAIMS

1. A purified and isolated DNA having a sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:51.
- 5 2. A purified and isolated protein encoded by a gene whose sequence includes a sequence selected from the group consisting of SEQ ID NO:52 through SEQ ID NO:102.
- 10 3. A purified and isolated DNA having a sequence selected from the group consisting of SEQ ID NO: 103 through SEQ ID NO: 154.
- 15 4. A purified and isolated protein encoded by a gene sequence selected from the group consisting of SEQ ID NO: 155 through SEQ ID NO: 206.
- 20 5. A purified and isolated protein having an amino acid sequence selected from the group consisting of SEQ ID NO:52 through SEQ ID NO:102 and SEQ ID NO:155 through SEQ ID NO:206.
- 25 6. A method for the recombinant DNA-directed synthesis of a protein, said method comprising:
culturing a transformed or transfected host organism containing a DNA sequence capable of directing the host organism to produce said protein under conditions such that the protein is produced, said protein exhibiting substantial homology to a protein comprising the amino acid sequence selected from the group consisting of SEQ ID NO:52 through SEQ ID NO:102 or SEQ ID NO:155 through SEQ ID NO:206.
- 30 7. The method of claim 6, wherein the host
- 35

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- ° organism is transfected with a recombinant eukaryotic expression vector.

8. The method of claim 7, wherein the host organism is a eukaryotic cell.

5

9. A recombinant expression vector comprising a DNA sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:51 and SEQ ID NO:103 through SEQ ID NO:154.

10

10. A host organism transformed or transfected with a recombinant expression vector according to claim 9.

11. A method of detecting antibodies against HCV, said method comprising:

15

- (a) contacting a biological sample with at least one protein of claim 5 to form an immune complex with the antibodies; and
- (b) detecting the presence of the immune complex.

20

12. The method of claim 11 wherein the biological sample is selected from the group consisting of serum, saliva or lymphocytes or other mononuclear cells.

25

13. The method of claim 11, wherein the recombinant protein is bound to a solid support.

14. The method of claim 11, wherein the immune complex is detected using a labeled antibody.

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15. A hepatitis C virus kit comprising: at least one protein comprising an amino acid sequence selected from the group consisting of: SEQ ID NO:52 through SEQ ID NO:102 and SEQ ID NO:155 through SEQ ID NO:206.

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16. A composition comprising at least one recombinant protein of claim 5 and an excipient, diluent or carrier.

17. A composition comprising an expression vector capable of directing host organism synthesis of a protein having an amino acid sequence selected from the group consisting of SEQ ID NO: 52 through SEQ ID NO: 102 and SEQ ID NO: 155 through SEQ ID NO: 206.

18. A method of preventing hepatitis C infection, comprising administering the composition of claim 16 or 17 to a mammal in an effective amount to stimulate the production of protective antibody.

19. A vaccine for immunizing a mammal against hepatitis C infection, comprising at least one protein according to claim 5 in a pharmacologically acceptable carrier.

20. A vaccine for immunizing a mammal against hepatitis C infection, said vaccine comprising an expression vector capable of directing host organism synthesis of a protein having an amino acid sequence selected from the group consisting of SEQ ID NO:52 - SEQ ID NO:102 and SEQ ID NO:155 - SEQ ID NO:206.

21. A method for detecting the presence of the hepatitis C virus via a reverse transcription-polymerase chain reaction, said method comprising amplifying an HCV reverse transcription product by polymerase chain reaction using universal primers.

22. The method of claim 21, wherein said universal primers are deduced from universally conserved nucleotide domains found in SEQ ID NO: 1 through SEQ ID NO:

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- ° 51, in SEQ ID NO: 103 through SEQ ID NO: 154, or in consensus sequences shown in Figures 1A-H and 6A-K.

23. Substantially isolated and purified universal primers, wherein said primers have nucleic acid sequences derived from universally conserved nucleotide domains found in SEQ ID NO:1 through SEQ ID NO:51, in SEQ ID NO:103 through SEQ ID NO:154 and in consensus sequences showing Figures 1A-H and 6A-K.

10. 24. A diagnostic kit for use in detecting the presence of hepatitis C virus in a biological sample, said kit comprising at least two universal primers according to claim 22.

15. 25. A diagnostic kit for use in detecting the presence of hepatitis C virus in a biological sample, said kit comprising at least one nucleic acid sequence selected from the group consisting of SEQ ID No:1-51 or SEQ ID No:103-154.

20. 26. A method for determining the genotype of a hepatitis C virus, said method comprising:
amplifying reverse transcription
products of RNA via polymerase chain
25. reaction using genotype-specific
amplification primers deduced from
genotype-specific nucleotide domains
found in SEQ ID NO:1 through SEQ ID
NO:51, in SEQ ID NO:103 through SEQ ID
30. NO:154, or in consensus sequences shown
in Figures 1A-H and 6A-K.

27. A method for determining the genotype of a hepatitis C virus, said method comprising:
35. (a) amplifying RNA via reverse

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- transcription-polymerase chain reaction to produce amplification products;
- (b) contacting said products with at least one sequence shown in SEQ ID NO:1 through SEQ ID NO:51 and SEQ ID NO:103 through SEQ ID NO:154; and
- (c) detecting complexes of said product which bind to said nucleic acid sequence.

28. A method for determining the genotype of a hepatitis C virus, said method comprising:
- (a) amplifying RNA via reverse transcription-polymerase chain reaction to produce amplification products;
- (b) contacting said products with at least one genotype-specific oligonucleotide; and
- (c) detecting complexes of said products which bind to said oligonucleotide(s).

29. The method of claims 27 or 28, wherein said amplification of step (a) uses universal primers deduced from universally conserved nucleotide domains found in SEQ ID NO:1 through SEQ ID NO:51, in SEQ ID NO:103 through SEQ ID NO:154, or in consensus sequences shown in Figures 1A-H and 6A-K.

30. The method of claim 28, wherein said genotype-specific oligonucleotide of step (b) is a nucleic acid sequence deduced from genotype-specific nucleotide domains found in SEQ ID NO:1 through SEQ ID NO:51 and SEQ ID NO:103 through SEQ ID NO:154, or in consensus sequences shown in Figures 1A-H and 6A-K.

31. Substantially isolated and purified

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° genotype-specific oligonucleotides, wherein said oligonucleotides have nucleic acid sequences deduced from genotype-specific nucleotide domains found in SEQ ID NO:1 through SEQ ID NO:51, in SEQ ID NO:103 through SEQ ID NO:154, or in consensus sequences shown in Figures 1A-H and 5 6A-K.

32. Substantially purified and isolated genotype-specific peptides having amino acid sequences deduced from a genotype-specific amino acid domains located 10 in SEQ ID NO:52 through SEQ ID NO:102, in SEQ ID NO:155 through SEQ ID NO:206, or in consensus sequences shown in Figures 2A-H and 7A-K.

33. A method of detecting antibodies specific 15 for a single genotype of HCV, said method comprising:

- (a) contacting a biological sample with at least one peptide of claim 32 to form an immune complex with the antibodies, and
- 20 (b) detecting the presence of the immune complex.

34. The method of claim 33, wherein the biological sample is selected from the group consisting of 25 serum, saliva or lymphocytes or other mononuclear cells.

35. The method of claim 33, wherein said peptide is bound to a solid support.

30 36. The method of claim 33, wherein the immune complex is detected using a labelled antibody or antigen.

37. A kit for use in detecting antibodies specific for a single genotype of HCV, said kit comprising: 35 at least one peptide selected from the genotype-specific

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° peptides of claim 32.

38. Substantially purified and isolated universal peptides having amino acid sequences deduced from universally conserved amino acid domains found in SEQ ID NO:52 through SEQ ID NO:102, in SEQ ID NO:155 through SEQ ID NO:206, or in consensus sequences shown in Figures 2A-H and 7A-K.

39. A method of detecting antibodies against all genotypes of HCV, said method comprising:

- (a) contacting a biological sample with at least one peptide of claim 38 to form an immune complex with the antibodies, and
- (b) detecting the presence of the immune complex.

40. The method of claim 39, wherein the biological sample is selected from the group consisting of serum, saliva or lymphocytes or other mononuclear cells.

41. The method of claim 39, wherein said peptide is bound to a solid support.

42. The method of claim 39, wherein the immune complex is detected using a labelled antibody or antigen.

43. A composition comprising at least one peptide of claim 32 and an excipient, diluent or carrier.

44. A composition comprising at least one peptide of claim 38 and an excipient, diluent or carrier.

45. A method of preventing hepatitis C infection, comprising administering the composition of

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- ° claims 43 or 44 to a mammal in an effective amount to stimulate production of a protective antibody.

46. A vaccine for immunizing a mammal against hepatitis C infection, comprising at least one peptide according to claims 32 or 38 in a pharmaceutically acceptable carrier.

47. A composition comprising at least one expression vector capable of directing host organism synthesis of a genotype-specific peptide having amino acid sequence deduced from a genotype-specific amino acid domain located in SEQ ID NO:52 - SEQ ID NO:102, and SEQ ID NO:155 - SEQ ID NO:206, or in consensus sequences shown in figures 2A-H and 7A-K.

48. A composition comprising at least one expression vector capable of directing host organism synthesis of a universal peptide having amino acid sequence deduced from universally conserved amino acid domains found in SEQ ID NO:52 - SEQ ID NO:102, and SEQ ID NO:155 - SEQ ID NO:206, or in consensus sequences shown in figures 2A-H and 7A-K.

49. A method of preventing hepatitis C infection, comprising administering the composition of claims 47 or 48 to a mammal in an effective amount to stimulate production of a protective antibody.

50. A vaccine for immunizing a mammal against hepatitis C infection, said vaccine comprising at least one expression vector capable of directing host organism synthesis of a geno-type specific peptide having amino acid sequence deduced from a geno type-specific amino acid domain located in SEQ ID NO:52 - SEQ ID NO:102, and SEQ ID NO:155 - SEQ ID NO:206, or in consensus sequences shown in

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° figures 2A-H and 7A-K.

51. A vaccine for immunizing a mammal against hepatitis C infection, comprising at least one expression vector capable of directing host organism synthesis of a universal peptide having amino acid sequence deduced from
5 universally conserved amino acid domain found in SEQ ID NO:52 - SEQ ID NO:102, and SEQ ID NO:155 - SEQ ID NO:206, or in consensus sequences shown in figures 2A-H and 7A-K.

10 52. Anti-HCV core antibodies having specific binding affinity for core protein of a single genotype of HCV.

15 53. Anti-HCV envelope 1 antibodies having specific binding affinity for envelope 1 protein of a single genotype of HCV.

20 54. The antibodies of claims 52 or 53 wherein said antibodies are monoclonal antibodies.

25 55. A method of detecting core protein specific for a single genotype of HCV, said method comprising:

- (a) contacting a biological sample with at least one antibody of claim 52 to form an immune complex with said core protein, and
- (b) detecting the presence of the immune complex.

30 56. A method of detecting E1 protein specific for a single genotype of HCV, said method comprising:

- (a) contacting a biological sample with at least one antibody of claim 53 to form an immune complex with said E1 protein; and
- 35

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- °
- (b) detecting the presence of the immune complex.

57. The methods of claims 55 or 56, wherein the biological sample is selected from the group consisting of serum, saliva lymphocytes or other mononuclear cells and liver.

58. The method of claims 55 or 56, wherein said antibody is bound to a solid support.

59. A method of detecting antibodies against all genotypes of HCV, said method comprising:

- (a) contacting a biological sample with at least one universal peptide of claim 38 to form an immune complex with said antibodies; and
- (b) detecting the presence of the immune complex.

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FIGURE 1A-1

SEQ ID NO:	Isolate
5	S14
1	DK7
8	US11
4	DR4
3	DR1
2	DK9
6	S18
7	SW1
1-8	consensus

1 TACCAAGTGGCAACTCCACGGGGCTTTACCATGTcACCAATGATtGCCCCTAACTCGAGTA
|||||
1 TACCAAGTGGCAACTCCACGGGGCTTTACCATGTcACCAATGATtGCCCCTAACTCGAGTA
|||||
1 TACCAAGTaCGCAACTCCACGGGGCTTTACCATGTcACCAATGATtGCCCCTAACTCGAGTA
|||||
1 CACCAAGTGGCAACTCTACAGGGCTTTACCATGTcACCAATGATtGCCCCTAACTCGAGTA
|||||
1 CACCAAGTGGCAACTCTACAGGGCTTTACCATGTcACCAATGATtGCCCCTAACTCGAGTA
|||||
1 TACCAAGTACGCAACTCctCGGGCCTcTACCATGTcACCAATGATtGCCCCTAACTCGAGTA
|||||
1 TACCAAGTACGCAACTCcaCGGGCCTTTACCATGTcACCAATGAcTGGCCCTAACTCGAGCA
|||||
1 TACCAAGTACGCAACTCctCGGGCCTTTACCATGTcACCAATGATtGCCCCTAACTCGAGTA
|||||
tACCAAGT-CGCAACTCcaCgGGgCTtTACCATGTcACCAATGATtGCCCCTAAcTCGAGTA

SEQ ID NO.	Isolate
5	S14
1	DK7
8	US11
4	DR4
3	DR1
2	DK9
6	S18
7	SW1
1-8	consensus

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FIGURE 1A-3

SEQ ID NO:	Isolate	
5	S14	123 GGGTAACacCTCGAGGTGTTGGGTGGCGATGACCCCCACCGTGGCCACcAGGGAcGGCAAA
1	DK7	123 GGGTAACGtCTCGAGGTGTTGGGTGGCGATGACCCCCACCGTGGCCACcAGGGAtGGCAAA
8	US11	123 GGGTAACGctTCGAGGTGTTGGGTGGCGATGACCCCCACCGTGGCCACcAGGGACGGCAAA
4	DR4	123 GGGTAACaCCTCGAGGTGTTGGGTGGCGTGACCCCCACCGTGGCCACcAGGGACGGCAAA
3	DR1	123 GGGTAACGCCTCGAGGTGTTGGGTGGCGTGACCCCCACCGTGGCCACcAGGGACGGCAAA
2	DK9	123 GGGTAACGCCCTCGAaATGTTGGGTGGCGTGGCCCCCACCAGTGGCCACcAGGGACGGCAAg
6	S18	123 GGGTAACGCCCTCGAgATGTTGGGTGcCGTGGCCCCCACCAGTtGCCACcAGGGACGGCAAA
7	SW1	123 GGaTggCGCCcCGAagTGTTGGGTGgCGGTGGCCCCCACCAGTcGCCACtAGGGACGGCAAA
1-8	consensus	GGGTaaGgcctCGAggTGTTGGGTGgCGGTGaCCCCCACCAGTgGCCACcAGGGACGGCAAA

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FIGURE 1A-4

SEQ ID NO:	Isolate	
5	S14	184 CTCCCCgCAaCGCAGCTTCGACGTTcACATCGATCTGCTtGTcGGGAGcGCCACCCCTCTGTT
1	DK7	184 CTCCCCACAGCGCAGCTTCGACGTCACATCGATCTGCTcGTcGGGAGtGCCACCCCTCTGTT
8	US11	184 CTCCCCACAACGCAaCTTCGACGTCACATCGATCTGCTTGTcGGGAGCGCCACCCCTCTGTT
4	DR4	184 CTCCCCACAACGCAgCTcCGACGTCACATCGACCTGCTTGTcGGGAGCGCCACCCCTCTGCT
3	DR1	184 CTCCCCACAACGCAgCTTCGACGTCACATCGACCTGCTTGTcGGGAGCGCCACCCCTCTGCT
2	DK9	184 CTCCCCGCAaCGCAGCTTCGACGTCACATCGATCTGCTTGTcGGGAGCGCCACCCCTCTGCT
6	S18	184 CTCCCCGCAaCGCAGCTTCGACGTCACATCGATCTGCTTGTtGGGAGCGCCACCCCTCTGCT
7	SW1	184 CTCCctGCAaCGCAGCTTCGACGTCACATCGATCTGCTTGTcGGaAGCGCCACCCCTCTGCT
1-8	consensus	CTCCCC - CAaCGCAgCTtCGACGTCACATCGAtCTGCTtGTcGGgAGcGCCACCCCTCTGcT

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FIGURE 1A-5

SEQ ID NO:	Isolate	
5	S14	245 CGGCCCTCTACGTGGGGACCTGTGCGGGTCTGTCTTCTTGTGCGGTCAgCTGTTTACCTT
1	DK7	245 CGGCCCTCTACGTGGGGACCTGTGCGGGTCTGTCTTCTTGTGCGGTCAACTGTTTACCTT
8	S11	245 CGGCCCTCTACGTGGGGACCTGTGCGGGTCTGTCTTCTTGTGCGGTCAACTGTTTACCTT
4	DR4	245 CGGCCCTCTACGTGGGGACCTGTGCGGGTCTGTCTTCTTGTGCGGTCAACTGTTTACCTT
3	DR1	245 CGGCCCTCTACGTGGGGACCTGTGCGGGTCTGTCTTCTTGTGCGGTCAACTGTTTACCTT
2	DK9	245 CGGCCCTCTATGTGGGGACCTGTGCGGGTCTGTCTTCTTGTGCGGCAACTGTTTACCTT
6	S18	245 CGGCCCTCTATGTGGGGACCTGTGCGGGTCTGTCTTCTTGTGCGGCAACTGTTTACCTT
7	SW1	245 CGGCCCTCTACGTGGGGACCTGTGCGGGTCTGTCTTCTTGTGCGGTCAACTGTTTACCTT
1-8	consensus	CGGCCCTCTACGTGGGGAC - TGTGCGGGTCTGTCTTCTTGTGCGGTCAACTGTTTACCTT

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FIGURE 1A-6

SEQ ID NO:	Isolate	
5	S14	306 CTCTCCAGGCGCctCTGGACGACGCAAGaCTGCAATtGTTCTATCTATCCcGGCCATATA
1	DK7	306 CTCTCCAGGCGCCACTGGACGACGCAAGGCTGCAATtGTTCTATCTATCCcGGCCATATA
8	S11	306 CTCTCCAGaCGCCACTGGACGACGCAgGGCTGCAATtGTTCTATCTATCCCGGCCATATA
4	DR4	306 CTCTCCAGGCaCCACTGGACAACGCAAGaCTGCAATtGTTCCaTCTATCCCGGCCATATA
3	DR1	306 tTCTCCAGGCGCCACTGGACAACGCAAGaCTGCAATtGTTCTATCTATCCCGGCCATATA
2	DK9	306 CTCCCCAGaCGCCACTGGACAACGCAAGaCTGCAACTGTTCTATCTACCCCGCCATAt
6	S18	306 CTCCCCAGGCGCCACTGGACAACGCAAGaCTGCAACTGTTCTATCTACCCCGGCCATATA
7	SW1	306 CTCCCCAGGCGCCACTGGACAACGCAAGaCTGtAACTGTTCTATCTAtCCCCGGCCACATA
1-8	consensus	cTctCCCAGgCgCCCaCTGGACaACGCAaGaCTGcAAtTGTTctAtCTAtCCCcGGCCAtAta

FIGURE 1A-7

SEQ ID NO:	Isolate	
5	S14	367 ACGGTCATCCGATGGCaTGGGATATGATGAACTGGTCCCCCTACgACGGCaCTGGTAG
1	DK7	367 ACGGTCACCGCATGGCgTGGGATATGATGAACTGGTCCCCCTACcACGGCGTTGGTAG
8	S11	367 ACGGTCACCGCATGGCaTGGGATATGATGAACTGGTCCCCCTACgCGGCGTTGGTgG
4	DR4	367 ACGGGcCACCGCATGGCgTGGGATATGATGAACTGGTCCCCCTACgACAGCGCTGGTAG
3	DR1	367 ACGGGaCACCGtATGGCaTGGGATATGATGAACTGGTCCCCCTACgACAGCGCTGGTAA
2	DK9	367 ACGGTCATCCGATGGCgTGGGATATGATGAACTGGTCCCCCTACagCAGCGCTGGTAA
6	S18	367 ACGGTCACCGtATGGCaTGGGATATGATGAACTGGTCCCCCTACAAcGCGtTGGTAA
7	SW1	367 ACGGTCACCGcATGGCaTGGGATATGATGAACTGGTCCCCCcACAACaGCGcTGGTAG
1-8	consensus	ACGGGtCACCGcATGGCaTGGGATATGATGAACTGGTCCCCCtACgAc-GCgcTGGTag

FIGURE 1A-8

SEQ ID NO:	Isolate	
5	S14	428 TAGCTCAGCTGCTCCGGATCCCaCAAGCCATCTTGGATATGATCGCTGGTGCTCACTGGGG
1	DK7	428 TAGCTCAGCTGCTCCGGATCCCGCAAGCCATCTTGGACATGATCGCTGGTGCTCACTGGGG
8	S11	428 TAGCTCAGCTGCTCCGGATCCCaCAAGCCATCTTGGACATGATCGCTGGTGCTCACTGGGG
4	DR4	428 TAGCTCAGCTGCTCCGGATCCCaCAAGCCATCTTGGACATGATCGCTGGTGCTGGCCACTGGGG
3	DR1	428 TGGCTCAGCTGCTCCGGATCCCaCAAGCCATCTTGGACATGATCGCTGGaGCCCACTGGGG
2	DK9	428 TGGCgCAGCTGCTCAGGATCCCGCAGGCCATCTTGGACATGATCGCTGGTGCTGGCCACTGGGG
6	S18	428 TAGCTCAGCTGCTCAGGgTCCCGCAAGCCGCTCTTGGACATGATCGCTGGTGCTGGCCACTGGGG
7	SW1	428 TAGCTCAGCTGCTCAGGaTCCCGCAAGCCGCTCTTGGACATGATCGCTGGTGCTGGCCCACTGGGG
1-8	consensus	TaGctCAGCTGCTCcGGaTCCC - CAaGCCaTCTTGGAcATGATCGCTGGtGccCACTGGGG

FIGURE 1A-9

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	489 AGTCCTaGCGGCATAGCGTATTtTCCATGGTGGGaAACTGGGGCAAGGTcCCTaGTgGTG
1	DK7	489 AGTCCTgGCGGCATAGCGTATTtTCCATGGTGGGAACtGGGGCAAGGTcCCTGGTAGTG
8	S11	489 AGTCCTAGCGGCATAGCGTATTtCTCCATGGTGGGAACtGGGGCAAGGTcCCTGGTAGTG
4	DR4	489 AGTCCTAGCGGCATAGCGTATTtCTCCATGGTGGGAACtGGGGCAAGGTcCCTGGTAGTG
3	DR1	489 AGTCCTAGCGGCATAGCGTATTtCTCCATGGTGGGAACtGGGGCAAGGTcCGTGGTAGTG
2	DK9	489 AGTCCTAGCGGCATAGCGTATTtCTCCATGGTGGGAACtGGGGCAAGGTcGTGGTgGTa
6	S18	489 AGTCCTAGCGGCATAGCGTATTtCTCCATGGcGGGAACtGGGGCAAGGTcCCTGcTAGTG
7	SW1	489 AGTCCTAGCGGCATAGCGTATTtCTCCATGGtGGGAACtGGGGCAAGGTcCCTGaTAGTG
1-8	consensus	AGTCCTaGCGGCATAGCGTATTtTCCATGGtGGGgAACTGGGGCAAGGTccTggTaGTg

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FIGURE A1-10

SEQ ID NO:	Isolate	
5	S14	550 CTGCTGCTATTGCCGGCGTtGACGCG
1	DK7	550 CTGCTGCTATTGCCGGCGTcGACGCG
8	US11	550 CTGCTGCTATTGCCGGCGTcGACGCG
4	DR4	550 CTGTTGCTGTTTGCCGGCGTtGATGCG
3	DR1	550 CTGTTGCTGTTTGCCGGCGTtGATGCG
2	DK9	550 CTGTTGCTGTTTaCCGGCGTcGATGCG
6	S18	550 CTGTTGCTGTTTGCCGGCGTcGATGCG
7	SW1	550 CTGTTGCTGTTTtCCGGCGTcGATGCG
1-8	consensus	CTGtTGCTgTtTtGCCGGCGTcGAtGCG

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FIGURE 1B-1

SEQ ID NO:	Isolate	
11	DK1	1 TATGAAGTGGCGCAACGTGTCCGGGGTGTTACCAcGTcACaAACGACTGCTCCAACTCAAGCA
24	T10	1 TATGAAGTGGCGCAACGTGTCCGGGaTGTTACCAcGTcACgAACGACTGCTCCAACTCAAGCA
10	D3	1 TATGAAGTGGCGCAACGTGTCCGGGGTGTTACCAcGTcACcAAcGTGTCTCCAACTCGAGCA
9	D1	1 TATGAAGTGGCGCAACGTGTCCGGGGTGTTACCAcGTcACGAACGACTGTCTCCAACTCGAGCA
14	HK5	1 TATGAAGTGGCGCAACGTGTCCGGGGTGTTACCAcGTcACGAACGACTGTCTCCAACTcAAGCA
15	HK8	1 TATGAAGTGGCGCAACGTGTCCGGGATATACCAcGTcACGAACGACTGTCTCCAACTCAAGCA
12	HK3	1 TATGAAGTGGCGCAACGTGTCCGGGATATACCAcGTcACGAACGACTGTCTCCAACTCAAGCg
23	T3	1 TAcGAAGTGGCGCAACGTGTCCGGGGTGTTAcTcATGTcACGAACGACTGTCTCCAACTCAAGCA
22	SW2	1 TATGAAGTGGCGCAACGTGTCCGGGGTGTTcCATGTcACGAACGACTGTCTCCAACTCAAGCA
17	IND8	1 TATGAgTGGCGCAACGTGTCCGGGGTGTTCCATGTcACGAACGACTGTCTCCAACTCAAGTA
16	IND5	1 TATGAAGTGGCGCAACGTGTCCGGGGTGTTACCAcGTcACGAACGACTGTCTCCAACTCAAGTA
21	SA10	1 TATGAAGTGGCGCAACGTGTCCGGGaTGTTACCAcGTcACGAACGACTGTCTCCAACTCAAGCA
20	S45	1 TATGAAGTGGCGCAACGTGTCCGGGgcGTACCAcGTcACGAACGACTGTCTCCAACTCAAGCA
25	US6	1 TATGAAGTGGCGCAACGTGTCCGGGATGTACCAcGTcACGAACGACTGTCTCCAACTCAAGCA
13	HK4	1 cATGAAGTGCaCAACGTATcCCGGGATcTACCAcGTcACGAACGACTGTCTCCAACTCAAGTA
18	P10	1 TATGAAGTGGCGCAACGTgTCCGGGGTGTTACCAcGTcACGAACGACTGTCTCCAACTCAAGTA
19	S9	1 TATGAAGTGGCGCAACGTATcCCGGGgcGTACCAcGTcACGAACGACTGTCTCCAACTCAAGTA
9-25	consensus	tAtGAaGTGcGcCAACGTgTCCGGGGgtgTAccAtGTcACgAaACGACTGcTCCAACTcAAGca

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FIGURE 1B-2

SEQ ID NO:	Isolate	
11	DK1	62 TcGTGTaTGAGGCAGtGGACgTGATCATGCaTACCCaGGGTGCGTGCCCTGCGTTcGGGA
24	T10	62 TtGTGtTcTGAGGCAGCGGACtTGATCATGCACACCCCGGGTGCGTGCCCTGCGTTcGGGA
10	D3	62 TcGTGTATGAGACAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTcGGGA
9	D1	62 TtGTGTATGAGACAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTcGGGA
14	HK5	62 TCGTGTAcGAGACaACGGACATGATCATGCACACCCCTGGGTGCGTGCCCTGCGTTcGGGA
15	HK8	62 TCGTGTATGAaACAGCGGACATGATtATGCATACCCCTGGATGCaTGCCCTGCGTTcGGGA
12	HK3	62 TCGTGTATGAGACAGCaGACATGATCATGCATACCCCTGGATGCGTGCCCTGCGTaCGGA
23	T3	62 TTGTGTATGAGACAGCGGACATGATCATGCACACCCCTGGGTGCGTGCCCTGCGTTcGGGA
22	SW2	62 TTGTGTATGAGACAGCGGACATGATCATGCATACCCCGGGTGCGTGCCCTGCGTTcGGGA
17	IND8	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTcGGGA
16	IND5	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACtCCCGGGTGCGTGCCCTGCGTTcGGGA
21	SA10	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTcGGGA
20	S45	62 TTGTGTATGAGGCAGtGGACgTGATCcTGACACCCCTGGGTGCGTGCCCTGCGTTcGGGA
25	US6	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACtCCCGGGTGCGTGCCCTGtGTcGGGA
13	HK4	62 TTGTGTATGAGGCAGCGGACATGATCATGCATACCCCGGGTGCGTGCCCTGcGTcGGGA
18	P10	62 TTGTGTATGAGGCAGCGGACATGATaATGCACACCCCGGGTGCGTGCCCTGtGTcGGGA
19	S9	62 TTGTGTAcGAGGCAGCGGACgTGATcATGCATACCCCGGGTGtGTaCCCTGcGTTCaGGA
9-25	consensus	TtGTGTatGAggCagcgGACaTGATcaTGCAcAcCccGGgTgcgTgCCCCTgcGTtCgGGA

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FIGURE 1B-3

SEQ ID NO:	Isolate	
11	DK1	123 GaaCAACcaCTCCCGtTGCTGGGTAGCGCTCACccccACGCTCGCGGCCAGGAACgCCAGC
24	T10	123 GGGCAACTCCTCCCGCTGTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACACCCAGC
10	D3	123 GGACAACTCCTCTCGCTGTGGGTAGCGCTCACCCCCACGCTCGCGGGCTAGGAATAGCAGC
9	D1	123 GGACAACTCCTCTCGCTGTGGGTAGCGCTCACCCCCACGCTCGCGGGCTAGGAATGGCAaC
14	HK5	123 aAACAACTCCTCCCGTTGtTGGGTAGCGCTcgCCCCACGCTCGCGGCCaAGGAACgCcCAGC
15	HK8	123 GAACAACTCCTCCCGTTGcTGGGTgGCGCTCACTCCCACGCTCGCGGGCTAGGAAtGTCAGC
12	HK3	123 GAACAACTCCTCCCGCTGtTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGTCAGC
23	T3	123 GAgCAAtTCCTCCCGCTGCTGGGTAGCGCTtACTCCCACGCTCGCGGCCAGGAACGCCAGC
22	SW2	123 GGcCAACTCCTCCCGCTGTGGGTAGCGCTCACTCCCACGCTaGCaGCCAGGAACaCCAGC
17	IND8	123 GGGCAACTtCTCTaGtTGCTGGGTAGCGCTCACTCCCACtTCTCGCGGGCTAGGAACGCCAGC
16	IND5	123 GGGCAACTCCTCTCGCTGTGGGTAGCGCTCACTCCCACtTCTCGCGGGCCAGGAACGCCAGC
21	SA10	123 GAACAACTCCTCCCGCTGTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACtCCAGC
20	S45	123 GAACAACTCCTCCCGtTGCTGGGTgGCGCTCACTCCCACGCTCGCGGCCAGGAACtCCAGC
25	US6	123 GAACAAtTCCTCCCGcTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGctAGC
13	HK4	123 GAACAACTCCTCCCGtTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGCCAGC
18	P10	123 GAACAACTCCTCCCGcTGCTGGGTAGCGCTCACTCCCACaCTCGCGGGCTAGGAAttCCAGC
19	S9	123 GggtAACTCCTCCCAaTGCTGGGTgGCGCTCAcCCCCACGCTCGCGGGCcAGGAACgCtAcC
9-25	consensus	gaacAActcCTCccgcTGcTGGGTaGGCTcaCtCCCACGCTcCGGGCcAGGAACgcccAgC

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FIGURE 1B-4

SEQ ID NO:	Isolate	
11	DK1	184 aTCCCCACTACGACaATACGACGCCATGTGCTCGATTGCTCGTTGGGCGGCTGCTTTCTGCT
24	T10	184 GTCCCCACTACGACgATACGACGCCATGTGCTCGATTGCTCGTTGGGCGGCTGCTTTCTGCT
10	D3	184 GTCCCCACTACGACaATACGACGCCACGTCGATTGCTCGTTGGGCGGCTGCTTTCTGCT
9	D1	184 GTCCCCACTACGGCgATACGACGCCACGTCGATTGCTCGTTGGGCGGCTGCTTTCTGCT
14	HK5	184 GTCCCCACcACGGCAATACGACGCCACGTCGACTTGCTCGTTGGGCGGCTGCTTTCTGCT
15	HK8	184 GTCCCCACTACGACaATACGACGCCACGTCGACTTGCTCGTTGGGCGGCTGCTTTCTGCT
12	HK3	184 GTCCCCACcACGACAAATACGACGTCACGTCGACTTGCTCGTTGGGCGGCTGCTTTCTGCT
23	T3	184 GTCCCCACTAaGACAAATACGACGTCACGTCGACTTGCTCGTTGGGCGGCTGCTTTCTGCT
22	SW2	184 GTCCCCACTACGACAAATACGACGCCACGTCGATTGCTCGTTGGGCGGCTGCTTTCTGCT
17	IND8	184 GTCCCCACcACGACAAATACGACGCCACGTCGATTGCTCGTTGGGCGGCTGCTTTCTGCT
16	IND5	184 GTCTcCCACcACGACAAATACGACaCCACGTCGATTGCTCGTTGGGCGGCTGCTTTCTGCT
21	SA10	184 GTCCCCACTACGACAAATACGACGCCACGTCGATTGCTCGTTGGGCGGCTGCTTTCTGCT
20	S45	184 GTCCCCACTACGACAAATACGACGTCACGTCGATTGCTCGTTGGGCGGCTGCTTTCTGCT
25	US6	184 GTCCCCACTACGACAAATACGACGCCACGTCGATTGCTCGTTGGGCGGCTaCTTTCTGCT
13	HK4	184 aTCCCCACTACGACAAATACGACGCCATGTGCTCGTTGGGCGGCTGCTTTCTGCT
18	P10	184 GTCCCcACTACGgCAATACGACGCCATGTGCTCGTTGGGCGGCTGCTTTCTGCT
19	S9	184 GTCCCCcACcACGaCAATACGACGtCATGTGCTCGTTGGGCGGCTGCTTTCTGCT
9-25	consensus	gTCCcCcAcAcGaCaATACGACgcCAcGTCGATTTGCTCGTTGGGCGGCTgctTTCTGCT

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FIGURE 1B-5

SEQ ID NO:	Isolate	
11	DK1	245 CCGCTATGTACGTGGGGACCTCTGCGGATCcGTTTTCTCGTCTCTCAGCTGTTACCTT
24	T10	245 CCGCTATGTATGTGGGAGACCTCTGCGGATCTGTTTTCTCGTCTCTCAGCTGTTACCTT
10	D3	245 CCGCCATGTACGTGGGGGATCTtTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT
9	D1	245 CCGCCATGTACGTGGGGGATCTcTGCGGATCTGTTTTCCCTCaTCTCCCAGCTGTTACCCt
14	HK5	245 CCGCTATGTACGTGGGGGATCTtTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT
15	HK8	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT
12	HK3	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT
23	T3	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT
22	SW2	245 CCGtTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT
17	IND8	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT
16	IND5	245 CCGCTATGTACGTGGGGGATCTaTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT
21	SA10	245 CCGCcATGTACGTGGGGGAcCTCTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT
20	S45	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCTCGTCTCCCAGCTGTTACCTT
25	US6	245 CCGCTATGTACGTGGGGGAcCTCTGCGGgTccGTTTTCTCGTCTCCCAGCTGTTACCTT
13	HK4	245 CCGCcATGTACGTGGGgAGATCTCTGCGGATCTGTcTTCTCGTCTCCCAGtGTTACCTT
18	P10	245 CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTCtTCTCGTCTCCCAGCTGTTACCTT
19	S9	245 CCGCTATGTACGTGGGGGAcCTgTGCGGATCTGTTtTCCCTCaTCTCCCAGCTGTTACCaT
9-25	consensus	CCGctATGTACGTGGGgGATCTcTGCGGaTcTgttTCTCTcTcTCCAGcTGTTCACctT

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FIGURE 1B-7

SEQ ID NO:	Isolate	
11	DK1	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACCTGGTCaCCTACAACAGCCCTAGTGC
24	T10	367 TCAGGTCACCGCATGGCTTGGGAcATGATGATGAACCTGGTCGCCCTACAACAGCctCTAGTGG
10	D3	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACCTGGTCGCCCTACagCAGCCCCCTAGTGG
9	D1	367 ACAGGTCACCGcATGGCTTGGGATATGATGATGAACCTGGTCACCTACAACAGCCctTAGTGG
14	HK5	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACCTGGTCACCTACAACAGCCCCCTAGTGG
15	HK8	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACCTGGTCgCCcACAACAGCCCCCTAGTGG
12	HK3	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACCTGGTCcCCctACagCAGCCCCCTAGTGG
23	T3	367 aCAGGTCACCGcATGGCTTGGGATATGATGATGAACCTGGTCgCCcACAaCgGCaCTAGTGG
22	SW2	367 TCAGGTCACCGCATGGCTTGGGAcATGATGATGAACCTGGTCACCTACAGCaGCCCTgGTGG
17	IND8	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACCTGGTCACCTACAGcgGCCCTAGTGG
16	IND5	367 TCAGGTCACCGCATGGCcTGGGATATGATGATGAACCTGGTCACCTACAGCAGCCCCCTAGTGG
21	SA10	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACCTGGTCACCTACAaCAGCctCTAGTaG
20	S45	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACCTGGTCgCCCTACAGCAGCCctTAGTGG
25	US6	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAATGGTCACCTACAGCAGCCCCCTAGTGG
13	HK4	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACCTGGTCACCTACAGCAGCCCCCTAGTGG
18	P10	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACCTGGTCGCCcACAGCAGCCCCCTAGTGG
19	S9	367 aCAGGTCAtCGCATGGCcTGGGATATGATGATGAACCTGGTCGCCctACAaCAGCCCCCTAGTGG
9-25	consensus	tCAGGTCACCGcATGGCtTGGGATATGATGATGAACtGGTCaCCtACAGCaGCCcTaGTgg

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FIGURE 1B-8

SEQ. ID NO:	Isolate	
11	DK1	428 TaTCGCAGTTACTCCGgATCCCAAGCTGTcGTGGACATGGTgCgGGGGCCCACTGGGG
24	T10	428 TgTCGCAGTTACTCCGGATCCCAAGCTGTcCaTGGACATGGTgCaGGGGCCCACTGGGG
10	D3	428 TATCGCAGTTACTCCGGATCCCAAGCTGTcGTGGACATGGTGGCGGGGGCCCACTGGGG
9	D1	428 TATCGCAGTTACTCCGGATCCCAAGCTGTcCaTGGACATGGTGGCGGGGGCCCACTGGGG
14	HK5	428 TGTTCGCAGTTACTCCGGATCCCGCAAGCTGTcGTGGACATGGTgAGCGGGGGCCCACTGGGG
15	HK8	428 TGTTCGCAGTTACTCCGGATCCCGCAAGCTaTCGTGGACATGGTGGCGGGGGCCCACTGGGG
12	HK3	428 TGTTCGCAaTTACTCCGGATCCCGCAAGCTGTcGTGGACATGGTGGCGGGGGCCCACTGGGG
23	T3	428 TGTTCGCAGTTgCTCCGGATCCCAAGCTGTcGTGGACATGGTGGCGGGGGCCCACTGGGG
22	SW2	428 TATTCGCAGTTaCTCCGGATCCCAAGCTGTcGTGGACATGGTGGCGGGGGCCCACTGGGG
17	IND8	428 TATTCGCAGTTGCTCCGGATCCCAAGCTGTcGTGGATATGGTGGCGGGGGCCCACTGGGG
16	IND5	428 TATTCGCAGTTGCTCCGGATCCCAAGCTGTcGTGGATATGGTGGCGGGGGCCCACTGGGG
21	SA10	428 TATTCGCAGTTACTCCGGATCCCAAGCTaTCGTGGACATGGTGGCGGGGGCCCACTGGGG
20	S45	428 TATTCGCAGTTACTCCGGATCCCAAGCTGTcGTGGACATGGTGGCGGGGGCCCACTGGGG
25	US6	428 TATTCGCAGTTACTCCGGATCCCAAGCTGTcGTGGACATGGTGGCGGGGGCCCACTGGGG
13	HK4	428 TATTCGCAGTTACTCCGacTCCCAAGCTGTcGTGGACATGGTGGCGGGgAGCCCACTGGGG
18	P10	428 TgTCGCAGCTACTCCGGATCCCAAGCTaTcTGGATgTGGTGGCGGGGGCCCACTGGGG
19	S9	428 TaTCGCAGCTACTCCGGATCCCAAGCTgTcCaTGGATaTGGTGGCGGGGGCCCACTGGGG
9-25	consensus	TaTCGCAGtTaCTCCGgaTCCCaCAAGCTgTcGTGGAcATGGTgCgGGgGCCCACTGGGG

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FIGURE 1B-9

SEQ ID NO:	Isolate	
11	DK1	489 AGTCCTGGCGGCCTTGCCTACTACTCCATGGCGGGAACTGGGCCAAGGTTTAAATTGTG
24	T10	489 AGTCCTGGCGGCCTTGCCTACTATTCCATGGCGGGAACTGGGCTAAGGTTTAAATTGTG
10	D3	489 GGTCTGGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
9	D1	489 GGTCTGGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
14	HK5	489 GGTCTGGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
15	HK8	489 AGTCCTAGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
12	HK3	489 AGTCCTAGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
23	T3	489 AGTCCTGGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
22	SW2	489 AGTCCTGGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
17	IND8	489 AATCCTGGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
16	IND5	489 AATCCTGGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
21	SA10	489 AGTCCTAGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
20	S45	489 AGTCCTGGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
25	US6	489 AGTCCTGGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
13	HK4	489 AGTCCTAGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
18	P10	489 AGTCCTGGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
19	S9	489 AGTCCTGGCGGCCTTGCCTACTATTCCATGGTGGGAACTGGGCTAAGGTTTGAATTGTG
9-25	consensus	agTCCTgCGGGCCCTtGCcTACTAtTCCATGGtgGGgAACTGGGCTtAAGGTTtTgATTGTg

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FIGURE 1B-10

SEQ ID NO:	Isolate	
11	DK1	550 tTGCTACTCTTTGCCGGCGTTGATGGG
24	T10	550 ATGCTACTCTTTGCCGGCGTTGATGGG
10	D3	550 ATGCTACTCTTTGCTGGCGTcGACGGC
9	D1	550 ATGCTACTCTTTGCTGGCGTTGACGGC
14	HK5	550 ATGCTACTtTTTGCCGGCGTTGATGGG
15	HK8	550 ATGCTACTgTTTGCCGGCGTTGATGGG
12	HK3	550 ATGCTACTtTTTGCCGGCGTTGATGGG
23	T3	550 cTGCTACTCTTTGCCGGCGTTGATGGG
22	SW2	550 ATGCTACTCTTTGCTGGCGTTGACGGG
17	IND8	550 ATGCTACTCTTTGCCGGCGTTGACGGG
16	IND5	550 ATGCTACTCTTTGCCGGCGTTGACGGG
21	SA10	550 ATGCTACTCTTTGCCGGCGTTGACGGG
20	S45	550 ATGCTACTCTTTGCCGGCGTTGACGGG
25	US6	550 tTGCTACTCTTTGCCGGCGTTGACGGG
13	HK4	550 ATGCTACTCTTTGCCGGCGTTGACGGG
18	P10	550 ATGCTACTCTTTGCCGGCGTTGACGGa
19	S9	550 ATGCTACTtTTTGCTGGtGTTGACGGg
9-25	consensus	atGCTACTcTTTGCCcGGcGTTtGAcGGg

SEQ ID NO:	Isolate
26	T2
27	T4
28	T9
29	US10
26-29	consensus

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FIGURE 1C-2

<u>SEQ ID NO:</u>	<u>Isolate</u>
26	T2
27	T4
28	T9
29	US10
26-29	consensus

123 GGGAAATACATccCGaTGCTGGATACCGGTcaCACCAAAcGTGGCCGTGCGGCAGCCCCGGC
 |||||
 123 GGGAAATACATctCGGTGCTGGATACCGGTtTCACCAAAcGTGGCCGTGCGGCAGCCCCGGC
 |||||
 123 tGGAAAcgTCgCGGTGCTGGATACCGGTCTcGCCAAACGTaGCTGTGCAGCGGCTGGC
 |||||
 123 gGGAAAtaCaTctCGGTGCTGGATACCGGTCTCaCCAAAtGTgCcGTGCAGCGGCTGGC
 |||||
 gGGAAAtaCaTctCGGTGCTGGATACCGGTctCaCCAAAcGTgGCCGTGC - GC - GCC - GGC

<u>SEQ ID NO:</u>	<u>Isolate</u>
26	T2
27	T4
28	T9
29	US10
26-29	consensus

184 GctCTtACGCAGGGCTTGCGGACGCACATcGACATGGTTGTGATGTCCGCCACGCTCTGCT
 |||||
 184 GCCCTCAGCAGGGCTTGCGGACGCACATtGACATGGTTGTGATGTCCGCCACGCTCTGCT
 |||||
 184 GCCCTCAGCAGGGCTTGCGGACGCACATCGACATGGTTGTGATGTCCGCCACGCTCTGCT
 |||||
 184 GCCCTCAGCAGGGCTTGCGGAcTcACATCGACATGGTcGTGATGTCCGCCACGCTCTGCT
 |||||
 GCcCTcACGCAGGGCTTGCGGACgCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT

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FIGURE 1C-3

SEQ ID NO:	Isolate	
26	T2	245 CTGCCCTcTACGTGGGGACCTCTGCGCGGGGTGATGCTGCAGCCCAGATGTTcATtGT
27	T4	245 CTGCTCTtTACGTGGGGACCTCTGCGCGGGGTGATGCTGCAGCCCAGATGTTcATcGT
28	T9	245 CCGCTCTcTACGTGGGGAtCTCTGCGCGGGGTaATGCTCGCCGCTcAGATGTTcATTaT
29	US10	245 CCGCTCTtTACGTGGGGActTCTGCGGtGGGaTgATGCTCGCaGCCaAaATGTTcATTgT
26-29	consensus	C-GCtCT-TACGTGGGGAccTCTGCGGcGGGgTgATGCTCGCaGCCAgATGTTcATTgT
SEQ ID NO:	Isolate	
26	T2	306 CTCGCCGgACgcCACTGGTTTGTGCAAGaATGCAATTGCTCcATCTACCCcGGtACCATC
27	T4	306 CTCGCCGAACAtCACTGGTTTGTGCAAGAcTGCAATTGCTCtATCTACCCtGGcACCATC
28	T9	306 CTCGCCGcAgCACCACtGGTTTGTGcAGGAATGCAACTGCTCCATtTACCCtGGTACCATC
29	US10	306 CTCGCCGcgcCACCACtGTTTGTGcAGGAATGCAACTGCTCCATcTACCCcGGTACCATC
26-29	consensus	CTCGCCGC-aCacCACTgGTTTGTGCA-GAaTGCAa-TGCTCcATcTACCC-GGtACCATC

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FIGURE 1C-4

<u>SEQ ID NO:</u> 26	<u>Isolate</u> T2	367 ACTGGACACCGTATGGCATGGGACATGATGATGAACCTGGTCGCCCCACaGCCACCATGATCC
27	T4	367 ACTGGACACCGTATGGCATGGGACATGATGATGAACCTGGTCGCCCCACgGCCACCATGATCC
28	T9	367 ACTGGACACCGTATGGCATGGGACATGATGATGAACCTGGTCGCCCCACaaCCACCATGATCt
29	US10	367 ACcGGgCACCGTATGGCATGGGACATGATGATGAACCTGGTCGCCCCACgCCACcttTGATCc
26-29	consensus	ActGGaCACCGTATGGCATGGGACaATGATGATGAACCTGGTCGCCCCAC-gCCACCaTGATCc
<u>SEQ ID NO:</u> 26	<u>Isolate</u> T2	428 TGGCGTACGCGATGCGCGTTCCCGAGGTcATCaTAGACATCaTcgCGGGGGCtCACTGGGG
27	T4	428 TGGCGTACGCGATGCGCGTTCCCGAGGTcATCtTAGACATCgTtAGCGGGGCaCACTGGGG
28	T9	428 TGGCGTACGCGATGCGCGTTCCCGAGGTcATCaTAGACATCaTcAGCGGgGctCACTGGGG
29	US10	428 TGGCGTACGtGATGCGCGTTCCCGAGGTcATCaTAGACATCaTtAGCGGgGCgCAtTGGGG
26-29	consensus	TGGCGTACGcGATGCGCGTTCCCGAGGTcATCaTAGACATCaT-agCGGGgGctCAcTGGGG

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FIGURE 1C-5

SEQ. ID NO:	Isolate	
26	T2	489 CGTCATGTTtGGCTTGGCCCTACTTCTCTATGCAGGGAGCGTGGCGGAAGTCaTTGTTCATC
27	T4	489 CGTCATGTTcGGCTTGGCCCTACTTCTCTATGCAGGGAGCGTGGCGGAAGTcGTTGTTCATC
28	T9	489 CGTCATGTTcGGCCtTAGCCCTACTTCTCTATGCAGGGAGCGTGGCGGAAGTcGTTGTTCATC
29	US10	489 CGTctTGTTcGGctTAGCCCTACTTCTCTATGCAGGGAGCGTGGCGGAAGTcGTTGTTCATC
26-29	consensus	CGTCaTGTTcGGctT - GCCTACTTCTCTATGCAGGGAGCGTGGCGGA - GTCgTTGTTCATC
SEQ. ID NO:	Isolate	
26	T2	550 CTctTGCTGGCtGCTGGGGTGGACGCG
27	T4	550 CTtcTGCTGGCCGCTGGGGTGGACGCG
28	T9	550 CTgtTGCTcaCCGCTGGcGTGGACGCG
29	US10	550 CTtcTGCTagCCGCTGGgGTGGACGCG
26-29	consensus	CTt - TGCTggCcGCTGGgGTGGACGCG

[illegible]

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FIGURE 1D-2

<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	123 CAATGGCACCCCTGCGCTGCTGGATACAAGTaACACCTAATGTGGCTGTGAAACACCCGtGGC
30	DK8	123 CAATGGCACCCCTGCGCTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCCGCGGC
32	SW3	123 tAATGGCACCCCTGCACTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCCGCGGC
31	DK11	123 CAATGGCACCCCTGCACTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCCGCGGC
30-33	consensus	CAATGGCACCCtTGC-CTGCTGGATACAAGTgACACCTAATGTGGCTGTGAAACACCCGcGGC
<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	184 GCACTcACTCACAACCTGCGAAGcGCaTgTCGACGTGATCGTAATGGCAGCTACGGTCTGCT
30	DK8	184 GCACTtACTCaTAACTGCGAACAACACCGTCGACGTGATCGTAATGGCAGCTACGGTCTGCT
32	SW3	184 GCgCTCACTCACAACCTGCGAGCACACCGTCGATATGATCGTAATGGCAGCTACGGTCTGCT
31	DK11	184 GCaCTCACTCACAACCTGCGAGCACaTaGATATGATtGTAAATGGCAGCTACGGTCTGCT
30-33	consensus	GCaCTcACTCACAACCTGCGGA-CaCA-gTcGA--TGATcGTAAATGGCAGCTACGGTCTGCT

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FIGURE 1D-3

<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	245 CGGCCTTGTAATGTGGGgGACGTgTGCGGGGCCGTGATGATaGcGTGCGAGGCTtTCATAAAT
30	DK8	245 CGGCCTTGTAATGTGGGAGACGTaTGCGGGGCCGTGATGATCGTGTGCGAGGCTcTCATAAAT
32	SW3	245 CGGCCTTGTAATGTGGGAGACaTGTGCGGGGCCGTGATGATCGTGTGCGAGGCTtTCATAAAT
31	DK11	245 CGGCCTTGTAATGTGGGAGACgTGTGCGGGGCCGTGATGATCGTGTGCGAGGCTtTCATAgT
30-33	consensus	CGGCCTTGTAATGTGGGAGACgTgTGCGGGGCCGTGATGATcGtGTGCGAGGCTtTCATAaT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	306 ATCGCCaGAACGCCCAcAACTTcACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCATATC
30	DK8	306 ATCGCctGAACGCCCAcAACTTTACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCATATC
32	SW3	306 ATCGCCAGAAcGCCCAcAACTTTACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCgTATC
31	DK11	306 ATCGCCAGAAcCaCCACcAACTTTACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCacATC
30-33	consensus	ATCGCCaGAACgCCACaAACTtACCCA - GAGTGCAACTGTTCCATCTACCAAGGTCatATC

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FIGURE 1D-4

SEQ ID NO:	Isolate	
33	T8	367 ACCGGCCACCGCATGGCATGGGACATGATGCTgAACTGGTCACCAACTCTcACCATGATCC
30	DK8	367 ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC
32	SW3	367 ACCGGCCACCGCATGGCGTGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC
31	DK11	367 ACCGGCCACCGCATGGCaTGGGACATGATGCTtAACTGGTCACCAACTCTcACCATGATCC
30-33	consensus	ACCGGCCACCGCATGGCaTGGGACATGATGCTaAACTGGTCACCAACTCT - ACCATGATCC
SEQ ID NO:	Isolate	
33	T8	428 TCGCCTAcGctGCTCGTGTgCCTGAaCTAGtCCTtgAaGTTGTCTTCGGCGGCCCATTTGGGG
30	DK8	428 TCGCCTATGCCGCTCGTGTTCCTGAGCTAGcCCTccAgTTGTCTTCGGCGGCCCATTTGGGG
32	SW3	428 TtGCCTATGCCGCTCGTGTTCCTGAGCTAGTCCTTGAAGTTGTCTTCGGCGGCCCATTTGGGG
31	DK11	428 TcGCCTATGCCGccCGTGTTCCTGAGCTAGTCCTTGAAGTcGTCTTCGGtGGtCATTTGGGG
30-33	consensus	TcGCCTAtGccGctCGTGTtCCTGAgCTAGtCCTtgAaGTTGTCTTCGGcGGcCATTTGGGG

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FIGURE 1D-5

SEQ ID NO:	Isolate	
33	T8	489 CGTGGTGTGGCTTGGCCTATTCTCCATGCAaGGAGCGTGGGCCAAAGTCATcGCCATC
30	DK8	489 CGTGGTGTGGCTTGGCCTATTCTCCATGCAgGGAGCGTGGGCCAAAGTCATtGGCCATC
32	SW3	489 CGTGGTGTGGCTTGGCCTATTCTCCATGCAaGGAGCGTGGGCCAAAGTCATtGGCCATC
31	DK11	489 tGTGGTGTGGCTTGGCCTATTCTCCATGCAgGGAGCGTGGGCCAAAGTCATtGGCCATC
30-33	consensus	cGTGGTGTGGCTTGGCCTATTCTCCATGCA - GGAGCGTGGGCCAA - GTCATtGCCATC
SEQ ID NO:	Isolate	
33	T8	550 CTCCTcCTTGTCGcAGGAGTGGAcGCA
30	DK8	550 CTCCTtCTTGTCGcAGGAGTGGATGCA
32	SW3	550 CTCCTgCTTGTCGcAGGAGTGGATGCA
31	DK11	550 CTCCTtCTTGTAgCAGGAGTGGATGCA
30-33	consensus	CTCCTtCTTGTCGcAGGAGTGGAtGCA

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FIGURE 1E-1

<u>SEQ ID NO:</u>	<u>Isolate</u>	
35	DK12	1 tTAGAGTGGCGGAATGTGTCCGGCCTCTACGTCTTACCAACGACTGTtCCAATAGCAGTA
36	HK10	1 CTAGAGTGGCGGAATGTGTCTGGCCTCTATGTCTTACCAACGACTGTcCCAATAGCAGTA
37	S2	1 CTAGAGTGGCGGAATACGTCTGGCCTCTATGTCTcACCAACGACTGTTCCAATAGCAGTA
39	S54	1 CTAGAGTGGCGGAATACGTCTGGCCTCTATaTCCTTACCAACGACTGTTCCAATAGCAGTA
38	S52	1 CTAGAGTGGCGGAATACGTCTGGCCTCTATgTCCTTACCAACGACTGTTCCAATAGCAGTA
35-39	consensus	cTAGAGTGGCGGAATacGTCTcGGCCTCTAtgTCCTtACCAACGACTGTtCCAATAGCAGTA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
35	DK12	62 TcGTGTATGAGGCCGATGACGTcATTCTGCACACACCTGGCTGTGTACCTTGTGTTCAGGA
36	HK10	62 TTGTGTATGAGGCCGATGACGTcATTCTGCACACACCTGGCTGTGTACCTTGTGTTCAGGA
37	S2	62 TTGTGTATGAGGCCGATGACGTtATTCTGCACACACCTGGCTGTGTACCTTGTGTTCAGGA
39	S54	62 TTGTGTATGAGGCCGATGACGTcATTCTGCACACACCCGGCTGTGTACCTTGTGTTCAGGA
38	S52	62 TTGTGTATGAGGCCGATGACGTcATTCTGCACACACCCGGCTGTGTACCTTGTGTTCAGGA
35-39	consensus	TtGTGTATGAGGCCGATGACGTcATTCTGCACACACCTGGCTGTGTACCTTGTGTTCAGGA

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FIGURE 1E-2

SEQ ID NO:	Isolate	
35	DK12	123 CCGCAATACATCTACGTGCTGGACCTCaGTGACgCCTACAGTGGCAGTCAGGTACGTCGGA
36	HK10	123 CCGCAATACATCCACGTGCTGGACCTCgGTGACACCTACAGTGGCAGTCAGGTACGTCGGA
37	S2	123 CCGtAATACATCCACGTGCTGGACCCcAGTGACACCTACAGTGGCAGTCAGGTatGTCGGA
39	S54	123 CCGCAATACATCCACGTGCTGGACCCcAGTGACACCTACCGTGGCAGTCAGGTACGTCGGA
38	S52	123 CCGCAATACATCCatGTGCTGGACCCcAGTGACACCTACCGTGGCAGTCAGGTACGTCGGA
35-39	consensus	CGGcAATACATCcAcGTGCTGGACCCcCaGTGACaCCTACaGTGGCAGTCAGGTACGTCGGA
SEQ ID NO:	Isolate	
35	DK12	184 GCAACCAccGctTCGATACGCAGTCATGTGGACCTGcTAGTGGCGCGGCCACGATGTGCT
36	HK10	184 GCAACCAccGcTCGATACGCAGTCATGTGGACCTGTTAGTGGCGCGGCCACGATGTGCT
37	S2	184 GCAACCAccGCTTCGATACGCAGTCATGTGGACCTATTgTGGCGCGGCCACtATGTGCT
39	S54	184 GCAACCAccGCTTCGATACGCAGTCATGTGGACCTATTAGTGGCGCGGCCACGCTGTGCT
38	S52	184 GCAACCAccGCTTCGATACGCAGTCATGTGGACCTATTAGTGGCGCGGCCACGCTGTGCT
35-39	consensus	GCAACCAccGctTCGATACGCAGTCATGTGGACCTatTaGTGGCGCGGCCACgaTGTGCT

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FIGURE 1E-3

SEQ ID NO:	Isolate	
35	DK12	245 CTGGCGCTCTACGTGGGtGATgTGTGTGGGGCCGTCTTCCCTtGTGGGACAAAGCCTTcACGTT
36	HK10	
37	S2	245 CTGGCGCTCTACGTGGGcGATATGTGTGGGGCCGTCTTCCCTCGTGGGACAAAGCCTTcACGTT
39	S54	
38	S52	245 CTGGCGCTCTACGTGGGTGATATGTGTGGGGCCGTCTTCTCGTGGGACAAAGCCTTcACGTT
35-39	consensus	
		245 CTGGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTCTCGTGGGACAAAGCCTTcACGTT
		CTGGCGCTCTAcGTGGGtGATaTGTGTGGGGCCGTCTTtCTcGTGGGACAAAGCCTTcACGTT

SEQ ID NO:	Isolate	
35	DK12	306 CAGACcTcGTcGcCCATCAAAcCaGTcCAGAcCTGTAAcTGTcGTcGTAcCCAGGcCAcCTT
36	HK10	
37	S2	306 CAGAcCgGTcGcCCATCAAAcCGTcCAGAcCTGTAAcTGTcGTcGTAcCCAGGcCAcCTT
39	S54	
38	S52	306 CAGAcCTcGTcGcCCATCAAAcCGTcCAGAcCTGTAAcTGTcGTcGTAcCCAGGcCAcCTT
35-39	consensus	
		306 CAGAcCTcGTcGcCCATCAAAcCGTcCAGAcCTGTAAcTGTcGTcGTAcCCAGGcCAcCTT
		CAGAcCTcGTcGcCCATCAAAcCGTcCAGAcCTGTAAcTGTcGTcGTAcCCAGGcCAcCTT

FIGURE 1E-4

<u>SEQ ID NO:</u>	<u>Isolate</u>	
35	DK12	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCtGTGGGTATGGTGG
36	HK10	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCcGTGGGTATGGTGG
37	S2	367 TCAGGACATCGcATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
39	S54	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
38	S52	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
35-39	consensus	TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGCtGTGGGTATGGTGG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
35	DK12	428 TaGCGCACGTcCTGCGtCTGCCCCAGACCTTGTTCGACATAATAGctGGGGCCcATTGGGG
36	HK10	428 TGGCGCACGTcCTGCGgTTGCCCCAGACCTTGTTCGACATAATAGCGGGCCcATTGGGG
37	S2	428 TGGCGCACGTtCTGCGtTTGCCCCAGACcGTGTTCGACATAATAGCGGGCCcATTGGGG
39	S54	428 TGGCGCACATcCTGCGATTTGCCCCAGACCTTGTTCGACATACTGGCGGGCCcATTGGGG
38	S52	428 TGGCGCACATcCTGCGATTTGCCCCAGACCTTGTTCGACATACTGGCGGGCCcATTGGGG
35-39	consensus	TgGCGCACgTcCTGCG-tTGCCCCAGACCTTGTTCGACATAaTaGcGGGGCCcATTGGGG

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FIGURE 1E-5

SEQ ID NO:	Isolate
35	DK12
36	HK10
37	S2
39	S54
38	S52
35-39	consensus

489	CATCaTGGCgGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
489	CATCTTGGCaGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
489	CATCTTGGCGGGCCTAGCCTATTACTCCATGCaaGGCAACTGGGCCAAGGTCGCTATCATC
489	CATCTTGGCGGGCCTAGCCTATTATTCTATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
489	CATCTTGGCGGGCCTAGCCTATTATTCTATGCAGGGCAACTGGGCCAAGGTCGCTATTgTC
489	CATCtTGGCgGGCCTAGCCTATTAcTCCaATGCAGGGCAACTGGGCCAAGGTCGCTATCaTC

SEQ ID NO:	Isolate
35	DK12
36	HK10
37	S2
39	S54
38	S52
35-39	consensus

550	ATGGTTATGTTTTTCAGGaGTCGATGCC
550	ATGGTTATGTTTTTCAGGGGTCGATGCC
550	ATGGTTATGTTTTTCAGGGGTCGACGCC
550	ATGATTATGTTTTTCAGGGGTCGATGCC
550	ATGATTATGTTTTTCAGGGGTCGATGCC
550	ATGgTTATGTTTTTCAGGgGTCGAtGCC

FIGURE 1F-1

SEQ ID NO:	Isolate
43	Z7
42	Z6
42-43 consensus	(Z6)
43	Z7
42	Z6
42-43 consensus	(Z6)
43	Z7
42	Z6
42-43 consensus	(Z6)
43	Z7
42	Z6
42-43 consensus	(Z6)

SEQ ID NO:	Isolate
43	Z7
42	Z6
42-43 consensus	(Z6)
43	Z7
42	Z6
42-43 consensus	(Z6)
43	Z7
42	Z6
42-43 consensus	(Z6)
43	Z7
42	Z6
42-43 consensus	(Z6)

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FIGURE 1F-3

<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	489 taTCCTTaTcGGGgTGGCaTACTTctGCATGCAAGCTAAATTGGGCCAAGGTCATcCTGGTC
42	Z6	
42-43 consensus (Z6)		489 CgTCCTTgTTGGGtTGGCGTACTTCAGtATGCAAGCTAAATTGGGCCAAaGTcATCCCTGGTC
		cgTCCTTgTtGGGtTGGCGTACTTCaGtATGCAAGCTAAATTGGGCCAAaGTcATcCTGGTC

<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	550 CTTTTCCTCTcTaCGCTGGAGTTGATGCC
42	Z6	
42-43 consensus (Z6)		550 CTTTTCCTCTcTCGCTGGAGTTGATGCC
		CTTTTCCTCTcTCGCTGGAGTTGATGCC

SEQ ID NO:	Isolate	Sequence
45	SA1	62 TAGTCTACGAGGCTGATAgCCTGATctTGCACGCACCTGGcTGCGTGCCCTGTGTcAGGcA
47	SA5	62 TAGTCTACGAGGCTGATAACCTGATtCTGCACGCACCTGGTTGCGTGCCCTGTGTCAaGgA
49	SA7	62 TAGTCTAtGAGGCTGAcAACCTGATCCCTGCACGCACCTGGTTGCGTGCCCTGTGTcAGaCA
46	SA4	62 TAGTtTACGAGGCTGATAACCTGATCTTTGCAtGCACCTGGTTGCGTGCCctTGTGTcAGGCA
50	SA13	62 TcGTCTACGAGGCTGATGACCTGATCTTTACACGCACCTGGTTGCGTGCCCTGTGTtAGGCA
48	SA6	62 TaGTCTAtGAGGCTGATGACCTGATCcTACACGCACCTGGcTGCGTGCCCTGTGTcGGGaa
45 - 50	consensus	TaGtTcTAcGAGGCTGataaCCTGATc - TgCAcGCACCTGGtTGCGTGCCcCTGTGTcaggcA

FIGURE 1G-2

SEQ ID NO:	Isolate	Sequence
45	SA1	123 AGaTAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACaCTGTcAGCCCCCGAaCtTCGGA
47	SA5	123 AGgTAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACaTTGTcAGCCCCCGAAcCTCGGA
49	SA7	123 AaATAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACaTTGTcAGCCCCCGAAcCTCGGA
46	SA4	123 AGATAATGTCAGTAaGTGCTGGGTCCAAATCACCCCCACgTTGTcAGCCCCCGAAaCTCGGA
50	SA13	123 GGgTAATGTCAGTAGGTGCTGGGTCCAgATCACCCCCACaCTGTcAGCCCCCGAGcCTCGGA
48	SA6	123 GGaTAATGTCAGTAGaTGCTGGGTcCaTATCACCCCCACaCTaTCAGCCCCCGAGcCTCGGA
45 - 50	consensus	agaTAATGTCAGTAGgTGCTGGGTcCAaATCACCCCCACa - TgTCAGCCCCCGAaaccTCGGA

SEQ. ID NO.:	Isolate
45	SA1
47	SA5
49	SA7
46	SA4
50	SA13
48	SA6
45 - 50	consensus

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FIGURE 1G-3

SEQ ID NO:	Isolate	
45	SA1	245 CCGCACTATACGTCGGCGACCGCGTGGGGGCGAGTGTt cTGGTAGGCCAAATGTTACCTA
47	SA5	245 CCGCACTATACGTCGGGACCGCGTGGGGGCGAGTGTt cTGGTAGGCCAAATGTTACCTA
49	SA7	245 CCGCgCTATACGTCGGGACCGCGTGGGGGCGAGTGTtTGGTAGGCCAGATGTTcAgCTA
46	SA4	245 CCGCACTATACGTCGGGACCGCGTGGGGGCGAGTGTtTGGTAGGCCAAATGTTACCTA
50	SA13	245 CCGCGTTATACGTCGGAGACCGCGTGGGGGCGAGTGTtTGGTAGGtCAAATGTTACCTA
48	SA6	245 CCGCGTTATACGTCGGAGACGtGTGGGGGCAtTGtTtTGGTAGGcCAAATGTTACCTA
45-50	consensus	CCGC - cTATACGTCGGgGACGcGTGGGGGCGAgTGtTtTGGTAGGcCAaATGTTcAcCTA

SEQ ID NO:	Isolate	
45	SA1	306 TAGGCCTCGCCAGCATACcACaGTGCAGGACTGCAACTGTTCcATTACAGtGGCCATATC
47	SA5	306 TAGGCCTCGCCAGCATACTACGGTGCAGGACTGCAACTGTTCcATTACAGcGGCCATATC
49	SA7	306 TAGGCCTCGCCAGCACACTACGGTGCAGGACTGCAACTGTTCcATTACAGTGGCCATATC
46	SA4	306 TAGGCCTCGCCAGCACACTACGGTGCaAGACTGCAAtTGcTcATTACAGTGGCCATATC
50	SA13	306 TAGcCTCGCCgGCATaATgttGTGCAGGACTGCAACTGtTCCATTACAGTGGCCAcATC
48	SA6	306 TAGgCCTCGCCCaGCATgcTAcgGTaCAGGACTGCAACTGcTCCATTACAGTGGCCAtATC
45-50	consensus	TAGgCCTCGCCCaGCAtactacgGTgCAGgACTGCAAcTGtTCCATTACAGtGGCCAtATC

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FIGURE 1G-4

<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	367 ACCGGCCACCGgATGGcTTGGACATGATGAATTGGTCACCTACGACAGCCTTgCTGA
47	SA5	367 ACCGGCCACCGAATGGcATGGACATGATGAATTGGTCACCTACGACAGCCTTgGTGA
49	SA7	367 ACCGGCCACCGAATGGcATGGACATGATGAATTGGTCACCTACGACAGCCTTgGTGA
46	SA4	367 ACCGGCCACCGGATGGcATGGACATGATGAATTGGTCACCTACGAGcGCCTTgCTGA
50	SA13	367 ACCGGCCACCGGATGGcATGGACATGATGAATTGGTCACCTACaACAGcTTTgGTGA
48	SA6	367 ACTGGCCACCGGATGGcATGGACATGATGAATTGGTCACCCcgACAGCcTTTgGTGA
45-50	consensus	ACcGGCCACCGgATGGCaTGGGACATGATGAATTGGTCACcTaCgACaGcCTTgGTGA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
45	SA1	428 TGGCCcCAGaTGCTACGGATcCCCCAgGTGGTCATaGACATCATaGCCGGGGGCCACTGGGG
47	SA5	428 TGGCCcCAGgTGCTACGGATtCCCCAaGTGGTCATtGACATCATtGCCGGGGGCCACTGGGG
49	SA7	428 TGGCCcCAGTTGCTACGGATtCCCCAGGTGGTCATCGACATCATtGCCGGGGGCCACTGGGG
46	SA4	428 TGGCCcCAGTTGCTACGGATtCCCCAGGTGGTCATCGACATCATtGCCGGGGGCCACTGGGG
50	SA13	428 TGGCCcCAGTTGtTACGGATtCCCCAGGTGGTCATtGACATCATtGCCGGGGcCCACTGGGG
48	SA6	428 TGGCCcCAaATGcTACGGATtCCCCAGGTGGTCATtGACATCATtGCCGGGGgCCACTGGGG
45-50	consensus	TGGCCcCAGtTgCTACGGATtCCCCAGGTGGTCATtGACATCATtGCCGGGGgCCACTGGGG

FIGURE 1G-5

SEQ ID NO:	Isolate
45	SA1
47	SA5
49	SA7
46	SA4
50	SA13
48	SA6
45-50	consensus

SEQ ID NO:	Isolate	
45	SA1	550 CTGTTcCTGTTTGCGGGGTCGATGCC
47	SA5	550 CTGTTTCTGTTTGCGGGGTCGATGCC
49	SA7	550 TTGTTTCTGTTTGCGGGGTCGATGCC
46	SA4	550 TTGTTTCTGTTTGCGGGGTCGATGCC
50	SA13	550 cTGTTTCTGTTTGCGGGGTCGATGCC
48	SA6	550 tTGTTTCTGTTTGCGGGGTCGATGCC
45-50	consensus	-TGTTTCTGTTTGCGGGGTCGATGCC

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FIGURE 1H-1

SEQ ID NO:	Genotype
30-33	(IV/2b)
34	(2c)
26-29	(III/2a)
35-39	(V/3a)
9-25	(II/1b)
1-8	(I/1a)
40	(4a)
42-43	(4c)
44	(4d)
41	(4b)
45-50	(5a)
51	(6a)
1-51	consensus

1 GTGGAAGTcAGgAACAtCAGTTctAGcTACTAcGCCACCAATGATTGCTCaAACaCAGCA
 1 GTGGAGGTCAAGGACACCGGCGACTCCTACATGCCGACCAACGATTGCTCCAACTCTAGTA
 1 GcccAAGTGAagAACACCAgtacCaGcTACATGGTGACCAACGACTGtTCCAAAtGACAGCA
 1 cTAGAGTGGCGGAAtacGTctGGCCTCTAtgTCCtTACCAACGACTGtTCCAAAtAGCAGTA
 1 tAtGAaGTGcGCAACGTgTCCGGGgtgTaccAtGTCAcGAAcGACTGcTCCAACTcaAGca
 1 tACCAAGTgCGCAACTCcaCGGGCTtTACCATGTcACCAATGTATGCCCTAAcTCGAGtA
 1 GAGCACTACCGGAATGCTTCGGGCATCTATCACATCAcCAATGATTGTCCGAAATTCAGTA
 1 GTtAACTATcGCAATGCCCTCGGGCGTCTATCACgTCAcCAAGACTGCCCGAACTCGAGCA
 1 TACAACtATCGCAACAGCTCGGGTGTCTACCATGTCAcCAAGATtGCCCGAACTCGAGCA
 1 GTGCACTACCGGAATGCTTCGGGCGTCTATCATATGTCAcCAATGATTGCCCTAACACCAAGCA
 1 GTtCCcTACCGGAAtGCCCTcTGGGgtTAtCATGTcACCAATGATtGCCCaAACTctTCCA
 1 CTTACCTACGGCAACTCCAGTGGGCTATACCATCTCAcAAATGATTGCCCAACTCCAGCA

A TA AC AA GA TG C AA

SEQ ID NO:	Genotype
30-33	(IV/2b)
34	(2c)
26-29	(III/2a)
35-39	(V/3a)
9-25	(II/1b)
1-8	(I/1a)
40	(4a)
42-43	(4c)
44	(4d)
41	(4b)
45-50	(5a)
51	(6a)
1-51	consensus

62 TCACCTGGCAaCTCACCaaCGCAGTtCTCCACCTTCCCGGATGCGTCCCaTGTGAGAAATGA
 62 TCGTTTGGCAGCTTGAAGGAGCAGTGTCTTCACTACTCTGGATGCGTCCCTTGTGAGCGTAC
 62 TCACcTGGCAaCTccAgCcGGGTcCTCCACGTcCCCGGGTgTgTCCCGTgcGAGAAagt
 62 TtGTGTATGAGGCCGATGACGTcATTCTGCACACACcTGGTGTGTACCTTGTGTTCAGGA
 62 TtGTGTatGAggCagcgGACaTGATcaTGCAcACcCCcGGgTgCGTgCCCCGTTCGcGA
 62 TtGTGTACGAGgCGCCGATgCcATcCTgCACActCCgGGgTGTGTcCTTGGCTTCGcGA
 62 TAGTCTATGAAGCTGACCATCACATCTACACTTGCcGGGTGCGTACCCCTGTGTGATGAC
 62 TAGTGTATGAGGCCGAACACCAgATctTACACCTCCcAGGGTcTgCCCCGTGTGAGGGT
 62 TAGTCTATGAaACCGATTACCAcATCTTACACCTCCCGGGATGCCGTTCCTTGCCTGAGGGA
 62 TAGTGTACGAGACGGAGCACCACATCATGCACTTGCcAGGGTGTGTCCCCCTGTGTGCGGAC
 62 TaGTcTAcGAGGCTGAtaaCCTGATctTgCAcGCACCTGGtTGCCTGCCcTGTGTcagggca
 62 TCGTGTGGAGGGCGATGCTATGATCTTGCATTTGCCCTGGATGCTTGCCTTGTGTGAGGGT

T A T T CA CC GG TG T CC TG G

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FIGURE 1H-2

SEQ ID NO:	Genotype
30-33	(IV/2b)
34	(2c)
26-29	(III/2a)
35-39	(V/3a)
9-25	(II/1b)
1-8	(I/1a)
40	(4a)
42-43	(4c)
44	(4d)
41	(4b)
45-50	(5a)
51	(6a)
1-51	consensus

123 cAATGGCACCCcTGCgCTGCTGGATACAAGTgACACCTAAATGTGGCTGTGAAACACCGcGGC
 123 CGCCAACGTCTCTCGATGTTGGGTGCCGTTGCCCCCAAATCTGCCATAAGTCAACCTGGC
 123 gGGAATaCaTctCGtGTGTGGATACCGGTctCaCCAAACgTgGCcGTGCaGCaGCCCCGGC
 123 CGGCAATACATcCaAGTGTGGACcCaGTGACaCaCTACaGTGGCAGTCAGGTACGTCCGA
 123 gaacAAactcCTCccgCTGcTGGGTaGGCTcaCTCCACgCTcGGGcCaAGGAACgcccAgC
 123 GGgTaaCgctCGAggTGTGGGTGgCGGTGaCCCCCACgGTgGCCACcAGGACGGCAa
 123 TGGGAACACATCGCGTGTGGACGCCGCTGACGCCCTACAGTGGCTGTGCGCACACCCGGC
 123 tGGGAATCAGTCACGCTGTGGGTGGCCCTTACTCCACCCGCTGGCGGTGTCTATATCGGT
 123 AGGGAACAAGTCTACATGTGGGTGTCTCTACCCCCACCCGCTGGCGCAACATCTGAAT
 123 GGAGAATACTTCTCGCTGTGGGTGCCCTTGACCCCCACTGTGGCCCGCCCCCTATCCCCAAC
 123 agaTAATGTCAgTAggTGCTGGGTcCaAATCACCCCCACaTgTCAGCCCCGAaccTCGGA
 123 CGATGATCGGTCCACCTGTGGCATGTGTGACCCCCACCCCTGGCCATACCAAAATGCTTCC

TG TGG T C C C A T C

SEQ ID NO:	Genotype
30-33	(IV/2b)
34	(2c)
26-29	(III/2a)
35-39	(V/3a)
9-25	(II/1b)
1-8	(I/1a)
40	(4a)
42-43	(4c)
44	(4d)
41	(4b)
45-50	(5a)
51	(6a)
1-51	consensus

184 GCaCTcACTCaAACCTGCCAaCaCaTgTcGAcATGATcGTAATGGCAGCTACGGTCTGCT
 184 GCTCTCACTAAGGGCCTGCCAGCACACATCGATATCATCGTGTGTCTGTACGGTCTGT
 184 GCcCTcACGCAGGGCTTGCGGACgCACATcGACATGGTtGTGTGTCCGCCACGCTCTGCT
 184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTatTaGTGGCGCGGCCACgaTGTGCT
 184 gTCCcCaCtAcGaCaATACGACgCcACGTcGAtTTGCTCGTTGGGGCGGGTgctTTCTGCT
 184 CTCCCCgCaACGCAGCTtCGACGTcACATCGAtCTGCTtGTcGGgAGcGCCACCTCTGCT
 184 GCTCCGCTTGAGTCGTTCCGGCGACATGTGGACTTAATGGTAGCGCGGCCACTTTGTGTT
 184 GCTCCGCTTGACTCCcTCCGGAGACATGTGGACCTGATGGTgGGCGcGCTACTGtaTGCT
 184 GCTCCGCTTGAGTCTTTGAGACGTcACGTGGATCTGATGGTGGCGCGCCACTCTCTGCT
 184 GCACCGTTAGAGTCCATGGCAGGCAATGTAGACTGTATGGTGGGTGCGGCTACTATGTGTT
 184 GCGGTACGGCTCCTCTTCGGAGGGcCGTTGAcTACTaGCGGGaGGGcTGCcCTcTGCT
 184 ACGCCCGCAACGGGATTCCCGAGGCAATGTGGATCTTCTTCGGCGCGCCGCGAGTGGTTGCT

T G T GA T G GC T TG T

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FIGURE 1H-3

SEQ ID NO:	Genotype
30-33	(IV/2b)
34	(2c)
26-29	(III/2a)
35-39	(V/3a)
9-25	(II/1b)
1-8	(I/1a)
40	(4a)
42-43	(4c)
44	(4d)
41	(4b)
45-50	(5a)
51	(6a)
1-51	consensus

245 CGGCCTTGATGTGGGAGACgTgTGCGGGGCGGTGATGATcGtGTGCGAGGCTtTCATAaT
 245 CTGCCCTTTATGTGGGGAGCGTGTGTGGCGCGCTGATGCTGGCCGCTCAGGTCTGTCGTCGT
 245 CcGctCTtTACGTGGGGAGcCTCTGCGGCGGGgTgTGTCTCGCaGCCcAGATGTTCAAtgT
 245 CTGCGCTCTAcGTGGGTGATaTGTGTGGGGCCGTCTTtCTcGTGGGACAAGCCTTACAGTT
 245 CCGctATGTAcGTGGGGATCTcTGCGGaTcTGTtTCCtgTcTCCAGcTGTTCACctT
 245 CGGCCCTCTAcGTGGGGACtTGTGCGGGTCTGTCTTtCTtGTcGtCAaCTGTTcACctT
 245 CTGCCCTCTATGTTGGGGACCTCTGCGGAGGTGCCCTTCTGTATGGGCGAGATGATCACTTT
 245 CtGCCCTCTACgTTGGaGAtCTGTGCGGTGGtGcATTCTTGGTTGGcCAGATGTTcTcGTT
 245 CCGCCCTCTACATCGGAGACGTGTGTGGGGTGTGTCTTGGTGGTCAACTGTTACCTT
 245 CCGCTTCTACATTTGGAGATCTGTGTGGAGGCTCTTCCTAGTGGGCCAGCTGTTCCGACTT
 245 CCGGgcTATACGTGGGgGACGcGTGCGGGGCAgTGTtTtTGGTAGGcCAaATGTTCAcCTA
 245 CATCCCTGTACATCGGGGACCTGTGTGGCTCTCTCTTTTGGCGGGACAACtATTTCACCTT
 C T TA T GG GA TG GG T T CA T

SEQ ID NO:	Genotype
30-33	(IV/2b)
34	(2c)
26-29	(III/2a)
35-39	(V/3a)
9-25	(II/1b)
1-8	(I/1a)
40	(4a)
42-43	(4c)
44	(4d)
41	(4b)
45-50	(5a)
51	(6a)
1-51	consensus

306 ATCGCCaGAACgCCACaACTTtACCCaAGAGTGCAACTGTTCCATCTACCAAGGTcatATC
 306 GTCGCCACAACACCATACGTTTGTCCAGGAATGCAACTGTTCCATATACCCGGCCGcATT
 306 CTCGCCGCaacacCACTgTGTGTGCAAGaATGCAATTGCTCcATcTACCCtGGtACCATC
 306 CAGACctCGTCGCCATCAAAcGTCCAGACCTGTAACTGCTCGTGTACCCAGGCCAtcTT
 306 cTcGcCtCGcGgcAtgaGACagtaCAGgAcTGcAAcTGcTcaATCTATCCcGGcCacgTa
 306 cTctCCcAGgCgCCaCTGGACaACGCAAGaCTGcAAcTGTCTATCTATcCCGGCCAtATa
 306 TCGCCGCGTCCGCACTGGACCAcGAGGAGTGCAATTTGTTCCATCTACACTGGCCATATC
 306 CCAGCCGCGACGCCACTGGACTACGAGGACTGCAATTTGTTCTATCTACGCaGGGCAtaTc
 306 CCAACCTCGCCGCACTGGACCAcCCAGACTGCAATTTGTTCCATCTACACAGGACATATC
 306 CCGACCGCGCCGCACTGGACCAcCCAGGATTGCAACTGCTCCATCTATCTCTGGTCACGTC
 306 TAGcCTCGCCaGCAtactacgTgCAGGACTGCAACTGtTCCaTTTACAGtGGCCAtATC
 306 TCAGCCCCGCGCTCATTTGGACTGTGCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC
 CC C CA TG AA TG TC T TA GG T

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FIGURE 1H-4

SEQ ID NO:	Genotype
30-33	(IV/2b)
34	(2c)
26-29	(III/2a)
35-39	(V/3a)
9-25	(II/1b)
1-8	(I/1a)
40	(4a)
42-43	(4c)
44	(4d)
41	(4b)
45-50	(5a)
51	(6a)
1-51	consensus

367 ACCGGCCACCGCATGGCaTGGGACATGATGCTaAACTGGTCACCAACTCTtACCATGATCC
 367 ACGGACACCGCATGGCTTGGGATATGATGATGAACCTGGTGGCCCACTACCACTGCTCC
 367 ACTGGaCACCGTATGGCATGGGACATGATGATGAACCTGGTGGCCCACTGCTCC
 367 TCAGGACATCGaATGGCTTGGGATATGATGATGAATGGTGGCCCACTGCTCC
 367 tCAGGTCAcCGcATGGCTTGGGATATGATGATGAACCTGGTGGCCCACTGCTCC
 367 ACGGtCAcCGcATGGCaTGGGATATGATGATGAACCTGGTGGCCCACTGCTCC
 367 ACCGGCCACAGGATGGCTTGGGACATGATGATGAACCTGGAGCCCTACCACTCTGCTCC
 367 ACGGGCCACAGgATGGCaTGGGACATGATGATGAACCTGGAGTCCCACTGCTCC
 367 ACAGGACACAGaATGGCTTGGGACATGATGATGAATGGAGCCCTACCACTGCTCC
 367 TCGGGCCACAGGATGGCTTGGGACATGATGATGAACCTGGAGCCCTACCACTGCTCC
 367 ACcGGCCACCGgATGGCaTGGGACATGATGATGAATGGTCAcCtaCgACaGcCTTgTGA
 367 ACCGGCCACAGGATGGCTTGGGACATGATGATGAACCTGGTCAcCtaCgACaGcCTTgTGA
 C GG CA G ATGGC TGGGA ATGATG T AA TGG CC C T T

SEQ ID NO:	Genotype
30-33	(IV/2b)
34	(2c)
26-29	(III/2a)
35-39	(V/3a)
9-25	(II/1b)
1-8	(I/1a)
40	(4a)
42-43	(4c)
44	(4d)
41	(4b)
45-50	(5a)
51	(6a)
1-51	consensus

428 TcGCCTAtGcCGcTcGTGTtCCTGAgCTAGtCCTtGAAgTtGTCTTCGGcGGcCATTTGGGG
 428 TGGCGTACTTGGTGGCATCCCGGAAGTCATCTTGGATATTGTTACAGGAGGTCAATTGGGG
 428 TGGCGTACGcGATGCGCGTTCGGAGGTCAcTAGACATCaTtaGCGGgGCTCAcTTGGGG
 428 TgCGCACgTcCTCGctTGCCCCAGACCTTGTtGACATaATaGCCGGGGCCCATTTGGGG
 428 TaTCGCAGtTaCTCCGgaTCCCaCAAGCTgTCgTGGaCaTGGTgGCGGGGCCACTGGGG
 428 TaGctCAGCTGCTCcGgaTCCCGCAAGCCaTCTTGGaCaTGTATCGTGGtGcCaCTGGGG
 428 TCGCCcAGATCATGAGGGTCCcCACAGCCTTTCTCGACATGGTTGCCGAGGCCACTGGGG
 428 TCGCCcAGGTcATGAGGATCCCTAGCACTCTGGTAgATCTACTCgCTGGAGGGCACTGGGG
 428 TCGCCcAACTTATGAGGATCCcAGGCGCCATGGTCCAGCTGTCTTGCAGGCGGCCACTGGGG
 428 TGGCTCAGATCTTACGGATCCcCTCTATCCTAGGTGACTTGTCTACCGGGGGTCACTGGGG
 428 TGGCCcAgTtGcTACGGATtCCCCAgGTGGTCAcTgACATCAcTtCCCGGGgCCACTGGGG
 428 TATCTAGCATCTTGAAGGTACCTGAGATTTGTCCGAGTGTGATATTGTGGCCCATTTGGGG

T C G T CC T T GG G CA TGGGG

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FIGURE 2A-1

<u>SEQ ID NO:</u>	<u>Isolate</u>	
56	S14	1 YQVRNSTGLYHVTNDCPNSSIVYETADAILHaPGCVPCVREGNtSRCWVAMtPTVATRDGK
52	DK7	1 YQVRNSTGLYHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNvSRCWVAMtPTVATRDGK
59	US11	1 YQVRNSTGLYHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNaSRCWVAMtPTVATRDGK
55	DR4	1 HQVRNSTGLYHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNtSRCWVAVtPTVATRDGK
54	DR1	1 HQVRNSTGLYHVTNDCPNSSIVYEAADAILHaPGCVPCVREGNAsRCWVAVtPTVATRDGK
53	DK9	1 YQVRNSSGLYHVTNDCPNSSIVYEAADAILHSPGCVPCVREGNASKCWAVAPTVATRDGK
58	SW1	1 YQVRNSSGLYHVTNDCPNSSIVYETADAILHSPGCVPCVREDgApKCWVAVAPTVATRDGK
57	S18	1 YQVRNSTGLYHVTNDCPNSSIVYETADtILHSPGCVPCVREGnAsrCWVpVAPTVATRDGK
52-59	consensus	YQVRNSTGLYHVTNDCPNSSIVYEaADAILH-PGCVPCVREGnaSrCWVavtPTVATRDGK

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FIGURE 2A-3

SEQ ID NO:	Isolate	
56	S14	123 TGHMAWDMMNWSPTTALVVAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNNWAKVLVW
52	DK7	123 TGHMAWDMMNWSPTTALVVAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNNWAKVLVW
59	US11	123 TGHMAWDMMNWSPTaALVVAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNNWAKVLVW
55	DR4	123 TGHMAWDMMNWSPTTALVVAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNNWAKVLVW
54	DR1	123 TGHMAWDMMNWSPTTALVMAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNNWAKVVV
53	DK9	123 TGHMAWDMMNWSPTaALVMAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNNWAKVVV
58	SW1	123 TGHMAWDMMNWSPTTALVVAQLLRIPQAVLDMIAGAHWGVLAGIAYFSMVGNNWAKVLiV
57	S18	123 TGHMAWDMMNWSPTTALViAQLLRvPQAVLDMIAGAHWGVLAGIAYFSMaGNWAKVLiV
52-59	consensus	TGHMAWDMMNWSPTTALVVAQLLRiPQAILDMIAGAHWGVLAGIAYFSMVGNNWAKVLvV

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FIGURE 2A-4

<u>SEQ ID NO:</u>	<u>Isolate</u>	
56	S14	184 LLLFAGVDA
52	DK7	184 LLLFAGVDA
59	US11	184 LLLFAGVDA
55	DR4	184 LLLFAGVDA
54	DR1	184 LLLFAGVDA
53	DK9	184 LLLFtGVDA
58	SW1	184 LLLFsgVDA
57	S18	184 LLLFaGVDA
52-59	consensus	LLLFaGVDA

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FIGURE 2B-1

SEQ ID NO:	Isolate	
75	T10	1 YEVRNVSGmYHVTNDCSNSSIVfEaAdlIMHTPGCVPCVRegNsRCWVALTPTLAARNtS
62	DK1	1 YEVRNVSGvYHVTNDCSNSSIVYEAvDvIMHTPGCVPCVRENhSRCWVALTPTLAARNAS
64	HK4	1 hEhNVSGiYHVTNDCSNSSIVYEADmIMHTPGCVPCVRENSSRCWVALTPTLAARNAS
76	US6	1 YEVRNVSGmYHVTNDCSNSSIVYEADmIMHTPGCVPCVRENSSRCWVALTPTLAARNAS
68	IND8	1 YEVRNVSGvYHVTNDCSNSSIVYEADmIMHTPGCVPCVREGnfSsCWVALTPTLAARNAS
67	IND5	1 YEVRNVSGvYHVTNDCSNSSIVYEADmIMHTPGCVPCVREGNSSRCWVALTPTLAARNAS
73	SW2	1 YEVRNVSGvYHVTNDCSNSSIVYETAdmIMHTPGCVPCVREaNSSRCWVALTPTLAARNtS
63	HK3	1 YEVRNVSGiYHVTNDCSNSSvYETAdmIMHTPGCVPCVRENSSRCWVALTPTLAARNVS
66	HK8	1 YEVRNVSGiYHVTNDCSNSSIVYETAdmIMHTPGCmPCVRENSSRCWVALTPTLAARNVS
61	D3	1 YEVRNVSGVyqVTNDCSNSSIVYETAdmIMHTPGCVPCVREDnSSRCWVALTPTLAARNsS
74	T3	1 YEVRNVSGVyYVTNDCSNSSIVYETAdmIMHTPGCVPCVRESnSSRCWVALTPTLAARNAS
65	HK5	1 YEVRNVSGvYHVTNDCSNlSIVYETcDMIMHTPGCVPCVRENSSRCWVALaPTLAARNAS
71	S45	1 YEVRNVSGaYHVTNDCSNSSIVYEAvDvIlHTPGCVPCVRENSSRCWVALTPTLAARNSS
72	SA10	1 YEVRNVSGmYHVTNDCSNSSIVYEADmIMHTPGCVPCVRENSSRCWVALTPTLAARNSS
69	P10	1 YEVRNVSGvYHVTNDCSNSSIVYEADmIMHTPGCVPCVRENSSRCWVALTPTLAARNSS
60	D1	1 YEVRNVSGvYHVTNDCSNSSIVYETAdmIMHTPGCVPCVREDnSSRCWVALTPTLAARNgn
70	S9	1 YEVRNVSGaYHVTNDCSNSSIVYEADvIMHTPGCVPCVqEgNSSqCWVALTPTLAARNat
60-76	consensus	YEVRNVSGvYhVTNDCSNSSiVYEaAdmIMHTPGCVPCVrEnNsSrCWVALtPTLAARNas

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FIGURE 2B-2

SEQ ID NO:	Isolate	
75	T10	62 VPTTIRRHVDDL VGAAAFCSAMYVGDLCGSVFLVSQFLTFSPPRRHETIQDCNCsiYPGHl
62	DK1	62 IPTTIRRHVDDL VGAAAFCSAMYVGDLCGSVFLVSQFLTFSPPRRHETaQDCNCsiYPGHV
64	HK4	62 IPTTIRRHVDDL VGAAAFCSAMYVGDLCGSVFLVSQFLTFSPPRRHETVQDCNCsiYPGHV
76	US6	62 VPTTIRRHVDDL VGAAAtFCSAMYVGDLCGSVFLiSQFLTFSPPRqHETVQDCNCsiYPGHV
68	IND8	62 VPTTIRRHVDDL VGAAAFCSAMYVGDLCGSVFLVSQFLTFSPPRRHETVQDCNCsiYPGHV
67	IND5	62 VstTIRrhVDDL VGAAAFCSAMYVGDLCGSVFLVSQFLTFSPPRRHETVQDCNCsiYPGHV
73	SW2	62 VPTTIRRHVDDL VGAAAFCSvMYVGDLCGSVFLVSQFLTFSPPRRHETVQDCNCsiYPGHV
63	HK3	62 VPTTIRRHVDDL VGAAAFCSAMYVGDLCGSVFLVSQFLTFSPPRRHETVQDCNCsiYPGHV
66	HK8	62 VPTTIRRHVDDL VGAAAFCSAMYVGDLCGSVFLVSQFLTFSPPRRHETVQDCNCsiYPGHV
61	D3	62 VPTTIRRHVDDL VGAAAFCSAMYVGDLCGSVFLVSQFLTFSPPRRHETVQeCNCsiYPGHV
74	T3	62 VPTkTIRRHVDDL VGAAAFCSAMYVGDLCGSVFLVSQFLTFSPPRRHETVQDCNCsiYPGHV
65	HK5	62 VPTTaIRRHVDDL VGAAAFCSAMYVGDLCGSVFLVSQFLTFSPPRRHETVQDCNCsiYPGHV
71	S45	62 VPTTIRRHVDDL VGAAAFCSAMYVGDLCGSVFLVSQFLTFSPPRRHETVQDCNCsiYPGHV
72	SA10	62 VPTTIRRHVDDL VGAAAFCSAMYVGDLCGSVFLVSQFLTFSPPRryETVQDCNCsiYPGrv
69	P10	62 VPTTAIRRHVDDL VGAAAFCSAMYVGDLCGSVlVSQFLTFSPPRRHwTVQDCNCsiYPGHV
60	D1	62 VPTTAIRRHVDDL VGAAAFCSAMYVGDLCGSVFLiSQFLTlSPRRHETVQeCNCsiYPGHV
70	S9	62 VPTTtIRRHVDDL VGAAvFCSAMYVGDLCGSVFLiSQFLTtSPRRHETVQnCNCSiYPGHV
60-76	consensus	VpTttIRrhVDDL VGAAaAFCSaMYVGDLCGSvfLvSQFLTfSPRRheTvQdCNCSiYPGHv

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FIGURE 2B-3

SEQ ID NO:	Isolate	
75	T10	123 SGHRMAWDMMNWSPTTALVVSQLLRIPQAVmDMVtGAHWGVLAGLAYYSMAGNWAkVLIV
62	DK1	123 SGHRMAWDMMNWSPTTALV1SQLLRIPQAVvDMVAGAHWGVLAGLAYYSMAGNWAkVLIV
64	HK4	123 SGHRMAWDMMNWSPTAALVVSQLLR1PQAVMDMVAGAHWGVLAGLAYYSMVGNWAkVLIV
76	US6	123 SGHRMAWDMMNWSPTAALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAkVLIV
68	IND8	123 SGHRMAWDMMNWSPTAALVVSQLLRIPQAVVDMVAGAHGILAGLAYYSMVGNWAkVLIV
67	IND5	123 SGHRMAWDMMNWSPTAALVVSQLLRIPQAVVDMVAGAHGILAGLAYYSMVGNWAkVLIV
73	SW2	123 SGHRMAWDMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAkVLIV
63	HK3	123 SGHRMAWDMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAkVLIV
66	HK8	123 SGHRMAWDMMNWSPTtALVVSQLLRIPQAIvDMVAGAHWGVLAGLAYYSMVGNWAkVLIV
61	D3	123 TGHMAWDMMNWSPTaALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAkVLIV
74	T3	123 TGHMAWDMMNWSPTTALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAkVLIV
65	HK5	123 TGHMAWDMMNWSPTTALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAkVLIV
71	S45	123 TGHMAWDMMNWSPTaALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAkVLIV
72	SA10	123 TGHMAWDMMNWSPTtALVVSQLLRIPQAIvDMVAGAHWGVLAGLAYYSMVGNWAkVLIV
69	P10	123 sGHRMAWDMMNWSPTaALVVSQLLRIPQAI1DvVAGAHWGVLAGLAYYSMVGNWAkVLIV
60	D1	123 TGHMAWDMMNWSPTTALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAkVLIV
70	S9	123 TGHMAWDMMNWSPTTALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAkVLIV
60-76	consensus	SGHRMAWDMMNWSPTaALVVSQLLRiPQAVvDmVaGAHWGvLAGLAYYSMVGNWAkVLIV

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FIGURE 2B-4

<u>SEQ ID NO:</u>	<u>Isolate</u>	
75	T10	184 mLLFAGVDG
62	DK1	184 lLLFAGVDG
64	HK4	184 mLLFAGVDG
76	US6	184 lLLFAGVDG
68	IND8	184 MLLFAGVDG
67	IND5	184 MLLFAGVDG
73	SW2	184 MLLFAGVDG
63	HK3	184 MLLFAGVDG
66	HK8	184 MLLFAGVDG
61	D3	184 MLLFAGVDG
74	T3	184 lLLFAGVDG
65	HK5	184 MLLFAGVDG
71	S45	184 MLLFAGVDG
72	SA10	184 MLLFAGVDG
69	P10	184 MLLFAGVDG
60	D1	184 MLLFAGVDG
70	S9	184 MLLFAGVDG
60-76	consensus	mLLFAGVDG

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FIGURE 2C-1

<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	1 AQRNTsrgYMTNDCSNeSITWQLAAVLHVP GCiPCe r lGNTSRCWIPVtPNVAVRQPG
78	T4	1 AOVKNTtnSYMTNDCSNDsITWQLAAVLHVP GCVPCEKtGNTSRCWIPVSPNVAVRQPG
79	T9	1 AeVKNTSTSYMTNDCSNDsITWQLAAVLHVP GCVPCErVGNsSRCWIPVSPNVAVRQPG
80	US10	1 vqVKNTSTSYMTNDCSNDsITWQLAAVLHVP GCVPCEKvGNTSRCWIPVSPNVAVRQPG
77-80	consensus	aq'vKNTstSYMTNDCSNDsITWQLqAAVLHVP GCvPCE - vGNTSRCWIPVsPNVAV - - PG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	62 ALTQGLRTHIDMVVMSATLCSALYVGDLCGGVMLAAQMFIVSPrrHWFVQeCNCSiYPGTI
78	T4	62 ALTQGLRTHIDMVVMSATLCSALYVGDLCGGVMLAAQMFIVSPQHWFVQdCNCSiYPGTI
79	T9	62 ALTQGLRTHIDMVVMSATLCSALYVGDLCGGVMLAAQMFiiSPQHWFVQECNCSiYPGTI
80	US10	62 ALTQGLRTHIDMVVMSATLCSALYVGDfCGGmMLAAQMFIVSPrHHSFVQECNCSiYPGTI
77-80	consensus	ALTQGLRTHIDMVVMSATLCSALYVGDlCGGvMLAAQMFIVSP - hHwFVQeCNCSiYPGTI

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FIGURE 2C-2

<u>SEQ ID NO.:</u>	<u>Isolate</u>	
77	T2	123 TGHMAWDMMNWSPTATMILAYAMRVPEVIIdiigGAHWGVmFGLAYFSMQGAWAKViVI
78	T4	123 TGHMAWDMMNWSPTATMILAYAMRVPEVIIdiVSGAHWGVmFGLAYFSMQGAWAKVVVI
79	T9	123 TGHMAWDMMNWSPTtTMILAYAMRVPEVIIdiISGAHWGVmFGLAYFSMQGAWAKVVVI
80	US10	123 TGHMAWDMMNWSPTaTlILAYvMRVPEVIIdiISGAHWGVlFGLAYFSMQGAWAKVVVI
77-80	consensus	TGHMAWDMMNWSPTaTmILAYaMRVPEVIIdiISGAHWGVmFGLAYFSMQGAWAKVVVI

<u>SEQ ID NO.:</u>	<u>Isolate</u>	
77	T2	184 LLLAAGVDA
78	T4	184 LLLAAGVDA
79	T9	184 LLLtAGVDA
80	US10	184 LLLaAGVDA
77-80	consensus	LLLaAGVDA

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FIGURE 2D-1

<u>SEQ ID NO:</u>	<u>Isolate</u>	
82	DK11	1 VEVNtSSSYATNDCSNnSITWQLTNAVHLHLP GCVPCENDNGTLHCW IQVTPNVAVKHRG
83	SW3	1 VEVNtSSSYATNDCSNnSITWQLTNAVHLHLP GCVPCENDNGTLHCW IQVTPNVAVKHRG
84	T8	1 VEVNtSfSYATNDCSNnSITWQLTNAVHLHLP GCVPCENDNGTLRCW IQVTPNVAVKHRG
81	DK8	1 VEVNtSsSYATNDCSNnSITWQLTNAVHLHLP GCVPCENDNGTLRCW IQVTPNVAVKHRG
81-84	consensus	VEVRN-SsSYATNDCSNnSITWQLTNAVHLHLP GCVPCENDNGTL-CW IQVTPNVAVKHRG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
82	DK11	62 ALTHNLRAHidMIVMAATVCSALYVGDvCGAVMIVSQAFIvSPEhHfTQECNCsIYQGH I
83	SW3	62 ALTHNLRAHVDMIVMAATVCSALYVGDmCGAVMIVSQAFIISPERHNFTQECNCsIYQGr I
84	T8	62 ALTHNLRTHVDVIVMAATVCSALYVGDVCGAVMIaSQAFIISPERHNFTQECNCsIYQGH I
81	DK8	62 ALTHNLRTHVDVIVMAATVCSALYVGDVCGAVMIVSQALIIISPERHNFTQECNCsIYQGH I
81-84	consensus	ALTHNLR-HvD-IVMAATVCSALYVGDvCGAVMIVSQAFIISPERHnFTQECNCsIYQGH I

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FIGURE 2D-2

SEQ ID NO:	Isolate	
82	DK11	123 TGHMAWDMMLNWSPTLTMLAYAAARVPELVLEVFGGHGCVVFGFLAYFSMQGAWAKVIAI
83	SW3	123 TGHMAWDMMLNWSPTLTMLAYAAARVPELVLEVFGGHGCVVFGFLAYFSMQGAWAKVIAI
84	T8	123 TGHMAWDMMLNWSPTLTMLAYAAARVPELVLEVFGGHGCVVFGFLAYFSMQGAWAKVIAI
81	DK8	123 TGHMAWDMMLNWSPTLTMLAYAAARVPELVLEVFGGHGCVVFGFLAYFSMQGAWAKVIAI
81-84	consensus	TGHMAWDMMLNWSPTLTMLAYAAARVPELVLeVVFGGHGVVFGFLAYFSMQGAWAKVIAI

SEQ ID NO:	Isolate	
82	DK11	184 LLLVAGVDA
83	SW3	184 LLLVAGVDA
84	T8	184 LLLVAGVDA
81	DK8	184 LLLVAGVDA
81-84	consensus	LLLAVAGVDA

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FIGURE 2E-1

<u>SEQ ID NO:</u>	<u>Isolate</u>	
86	DK12	1 LEWRNVSGLYVLTNDCsNSSIVYEADDVILHTPGVPCVQDGNSTCWTSTVPTVAVRYVG
87	HK10	1 LEWRNVSGLYVLTNDCpNSSIVYEADDVILHTPGVPCVQDGNSTCWTSTVPTVAVRYVG
88	S2	1 LEWRNTSGLYVLTNDCSNSSIVYEADDVILHTPGVPCVQDGNSTCWTPTVPTVAVRYVG
90	S54	1 LEWRNTSGLYiLTNDCSNSSIVYEADDVILHTPGVPCVQDGNSTCWTPTVPTVAVRYVG
89	S52	1 LEWRNTSGLYvLTNDCSNSSIVYEADDVILHTPGVPCVQDGNSTmCWTPTVPTVAVRYVG
86 - 90	consensus	LEWRNtSGLYvLTNDCsNSSIVYEADDVILHTPGVPCVQDGNSTCWTpVTPTVAVRYVG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
86	DK12	62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
87	HK10	62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
88	S2	62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
90	S54	62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
89	S52	62 ATTASIRSHVDLLVGAATLCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHV
86 - 90	consensus	ATTASIRSHVDLLVGAATmCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHl

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FIGURE 2E-2

<u>SEQ ID NO:</u>	<u>Isolate</u>	
86	DK12	123 SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGImAGLAYYSMQGNWAKVAII
87	HK10	123 SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAII
88	S2	123 SGHRMAWDMMNWSPAVGMVVAHVLRLPQTVFDIIAGAHWGILAGLAYYSMQGNWAKVAII
90	S54	123 SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAII
89	S52	123 SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAIV
86-90	consensus	SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGILAGLAYYSMQGNWAKVAII

<u>SEQ ID NO:</u>	<u>Isolate</u>	
86	DK12	184 MVMFSGVDA
87	HK10	184 MVMFSGVDA
88	S2	184 MVMFSGVDA
90	S54	184 MIMFSGVDA
89	S52	184 MIMFSGVDA
86-90	consensus	MVMFSGVDA

SEQ ID NO:	Isolate	
93	Z7	1 VNYhNASGVYHiTNDCPNSSImYEAHHILHLP
94	Z6	1 VNYRNASGVYHVTNDCPNSSIVYEAHqILHLP
93-94 consensus	(Z6)	VNYrNASGVYHvTNDCPNSSIvYEAHqILHLP
93	Z7	62 APLeSiRRHVDLMVGAATVCSALYIGDL
94	Z6	62 APLdSLRRHVDLMVGAATVCSALYvGDL
93-94 consensus	(Z6)	APLdSLRRHVDLMVGAATVCSALYvGDL
93	Z7	123 TGHrMAWdMMNWSPTTLvLAQVMRIPSTL
94	Z6	123 TGHrMAWdMMNWSPTTLlLAQVMRIPSTL
93-94 consensus	(Z6)	TGHrMAWdMMNWSPTTLlLAQVMRIPSTL
93	Z7	184 LFLYAGVDA
94	Z6	184 LFLFAGVDA
93-94 consensus	(Z6)	LFLfAGVDA

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FIGURE 2G-1

SEQ ID NO:	Isolate	
98	SA5	1 VPYRNAGVYHVTNDPCPNSSIVYEADNLILHAPGCVPCVkegNVSRWCWVQITPTLSAPNLG
100	SA7	1 VPYRNAGVYHVTNDPCPNSSIVYEADNLILHAPGCVPCVRQnNVSRWCWVQITPTLSAPNLG
97	SA4	1 VPYRNAGVYHVTNDPCPNSSIVYEADNLILHAPGCVPCVRQDNVskCWVQITPTLSAPNLG
96	SA1	1 VPYRNAGVYHVTNDPCPNSSIVYEADsLILHAPGCVPCVRQDNVSRWCWVQITPTLSAPtfg
99	SA6	1 VPYRNAGVYHVTNDPCPNSSIVYEADDLILHAPGCVPCVRkDNVSRWCWhITPTLSAPSLG
101	SA13	1 VPYRNAGVYHVTNDPCPNSSIVYEADDLILHAPGCVPCVRqgNVSRWCWVqITPTLSAPSLG
96-101	consensus	VPYRNAGVYHVTNDPCPNSSIVYEADnLILHAPGCVPCVrqdNVsrCWVqITPTLSAPnlG

SEQ ID NO:	Isolate	
98	SA5	62 AVTAPLRRvVDYLAGGAALCSALYVGDAcGAVFLVGQMFtYRPRQHTTVQDCNCsIYSGHI
100	SA7	62 AVTAPLRRAVDYLAGGAALCSALYVGDAcGAVFLVGQMFsYRPRQHTTVQDCNCsIYSGHI
97	SA4	62 AVTAPLRRvVDYLAGGAALCSALYVGDAcGAVFLVGQMFYRPRQHTTVQDCNCsIYSGHI
96	SA1	62 AVTAPLRRvVDYLAGGAALCSALYVGDAcGAVFLVGQMFYRPRQHTTVQDCNCsIYSGHI
99	SA6	62 AVTAPLRRAVDYLAGGAALCSALYVGDVcGAlFLVGQMFYRPRQHaTVQDCNCsIYSGHI
101	SA13	62 AVTAPLRRvVDYLAGGAALCSALYVGDaCGAVFLVGQMFYsPRrHnvVQDCNCsIYSGHI
96-101	consensus	AVTAPLRRaVDYLAGGAALCSALYVGDaCGAVFLVGQMFtYrPRqHtTVQDCNCsIYSGHI

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FIGURE 2G-2

SEQ ID NO:	Isolate	
98	SA5	123 TGHMAWDMMNWSPPTALVMAQVLRIPQVVIDIAGGHGVLFAVAFASAANWAKVVLV
100	SA7	123 TGHMAWDMMNWSPPTALVMAQVLRIPQVVIDIAGGHGVLFAVAFASAANWAKVVLV
97	SA4	123 TGHMAWDMMNWSPPTALLMAQLLRIPQVVIDIAGGHGVLFAVAFASAANWAKVVLV
96	SA1	123 TGHMAWDMMNWSPPTALLMAQLLRIPQVVIDIAGGHGVLFAVAFASAANWAKVVLV
99	SA6	123 TGHMAWDMMNWSPaTALVMAQLLRIPQVVIDIAGGHGVLFAVAFASAANWAKVVLV
101	SA13	123 TGHMAWDMMNWSPtTALVMAQLLRIPQVVIDIAGGHGVLFAVAFASAANWAKVVLV
96-101	consensus	TGHMAWDMMNWSPtTALVMAQLLRIPQVVIDIAGGHGVLFAVAFASAANWAKVVLV
98	SA5	184 LFLFAGVDg
100	SA7	184 LFLFAGVDA
97	SA4	184 LFLFAGVDA
96	SA1	184 LFLFAGVDg
99	SA6	184 LFLFAGVDA
101	SA13	184 LFLFAGVDA
96-101	consensus	LFLFAGVDA

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FIGURE 2H-1

SEQ ID NO:	Genotype
81-84	(IV/2b)
85	(2c)
77-80	(III/2a)
86-90	(V/3a)
60-76	(II/1b)
52-59	(I/1a)
91	(4a)
93-94	(4c)
95	(4d)
92	(4b)
96-101	(5a)
102	(6a)
52-102	consensus

1 VEVNLSsSYATNDCSNnSITWQLTnAVLHLPGCVPCENDNGTLrCWIOVTPNVAVKHRG
 1 VEVKDTGDSYMPNTNDCSNSSIVWQLEGAVLHTPGCVPCERTANVSRCWVPVAPNLAISQPG
 1 aqVknTstSYMTNDCSNdSITWQLqAAVLHVPGCVpCEkvGNTSRCWIPVsPNVAVqqPG
 1 LEWRNtSGLYvLTNDCsNSSIVYEADDVILHTPGCVPCVDGNTStCWTPvTPTVAVRYVG
 1 YEVRNVSGvYhVTNDCSNsSiVyEaaDmImHTPGCVpCvErEnNsRcWVALtPTLAARNas
 1 YQVRNStGLYHVTNDCPNSSIVYEaADaILHsPGCVPCVREGnasrCWVavtPTVATRDKG
 1 EHYRNASGIYHITNDCPNSSIVYEADHILHLPGCVPCVMTGNTSRCTPvTPTVAVAHPG
 1 VNYrNASGVYHVTNDCPNSSIVYEAHqILHLPGCLPCVRvGNQSRCWVALTPTVAVsYIG
 1 YNYRNSSGVYHVTNDCPNSSIVYETDYHILHLPGCVPCVREGNKStCWVSLTPTVAAQHLN
 1 VHYRNASGVYHVTNDCPNStSIVYETEHHIMHLPGCVPCVrTENTSRCWVPLTPTVAApYPN
 1 VPYRNASGVYHVTNDCPNSSIVYEADnLILHAPGCVpCvrdNVsrCWVqITPTLSAPnLG
 1 LTYGNSSGLYHVTNDCPNSSIVLEADAMILHLPGCLPCVRVDDrStCWHAvtPTLAIPNAS

Y TNDC N S H PGC PC CW P

SEQ ID NO:	Genotype
81-84	(IV/2b)
85	(2c)
77-80	(III/2a)
86-90	(V/3a)
60-76	(II/1b)
52-59	(I/1a)
91	(4a)
93-94	(4c)
95	(4d)
92	(4b)
96-101	(5a)
102	(6a)
52-102	consensus

62 ALTHNLRthvDmIVMAATVCSALYVGdVCGAVMIVsQafIiSPeRhNFTQECNCsIYQGHl
 62 ALTKGLRAHIDIIVMSATVCSALYVGdVCGALMLAAQVVVSPQHHTFVQECNCsIYPGRl
 62 ALTQGLRTHIDMVMSATLCSALYVGdLlCGGvMLAAQMFIVSPqhHwFVQeCNCsIYPGTI
 62 ATTASIRSHVDLLVGAATmCSALYVGdMCGAVFLVGQAFTFRPRRHQTvQTCNCsLYPGHl
 62 vPtTtIRrHVDLLVGAAaFCSaMYVGDLCSGsvFlvSQLFTfSPRrheTvQdCNCsIYPGHv
 62 LPatQLRRhIDLVGsATLCSALYVGDLCSGsvFlvSQLFTfSPRrhwTtQdCNCsIYPGHl
 62 APLESFRRRHVDLMVGAATLCSALYVGDLCSGGAFLMGQMIFRPRRHWTtQECNCsIYTGHl
 62 APldSlRRRHVDLMVGAATVCSALYVGDLCSGGAFLVGOMFSFQPRRHWTtQdCNCsIYAGHl
 62 APLESRRRHVDLMVGAATLCSALYIGDVCGGVFLVGQLFTFQPRRHWTtQdCNCsIYTGHl
 62 APLESRRRHVDLMVGAATMCSAFYIGDLCSGGVFLVGQLFDfRPRRHWTtQdCNCsIYPGHV
 62 AVTAPLRaVDYLAGGAALCSALYVGDaCGAVFLVGQMftYrPRqhtVQdCNCsIYSGHl
 62 TPATGFRRHVDLLAGAAVVCSSLYIGDLCSGLFAGQLFTFQPRRHWTvQdCNCsIYTGHV

R D A CS Y GD CG Q P Q CNCs Y G

FIGURE 2H-2

SEQ ID NO:	Genotype	
81-84	(IV/2b)	184
85	(2c)	184
77-80	(III/2a)	184
86-90	(V/3a)	184
60-76	(II/1b)	184
52-59	(I/1a)	184
91	(4a)	184
93-94	(4c)	184
95	(4d)	184
92	(4b)	184
96-101	(5a)	184
102	(6a)	184
52-102	consensus	GV

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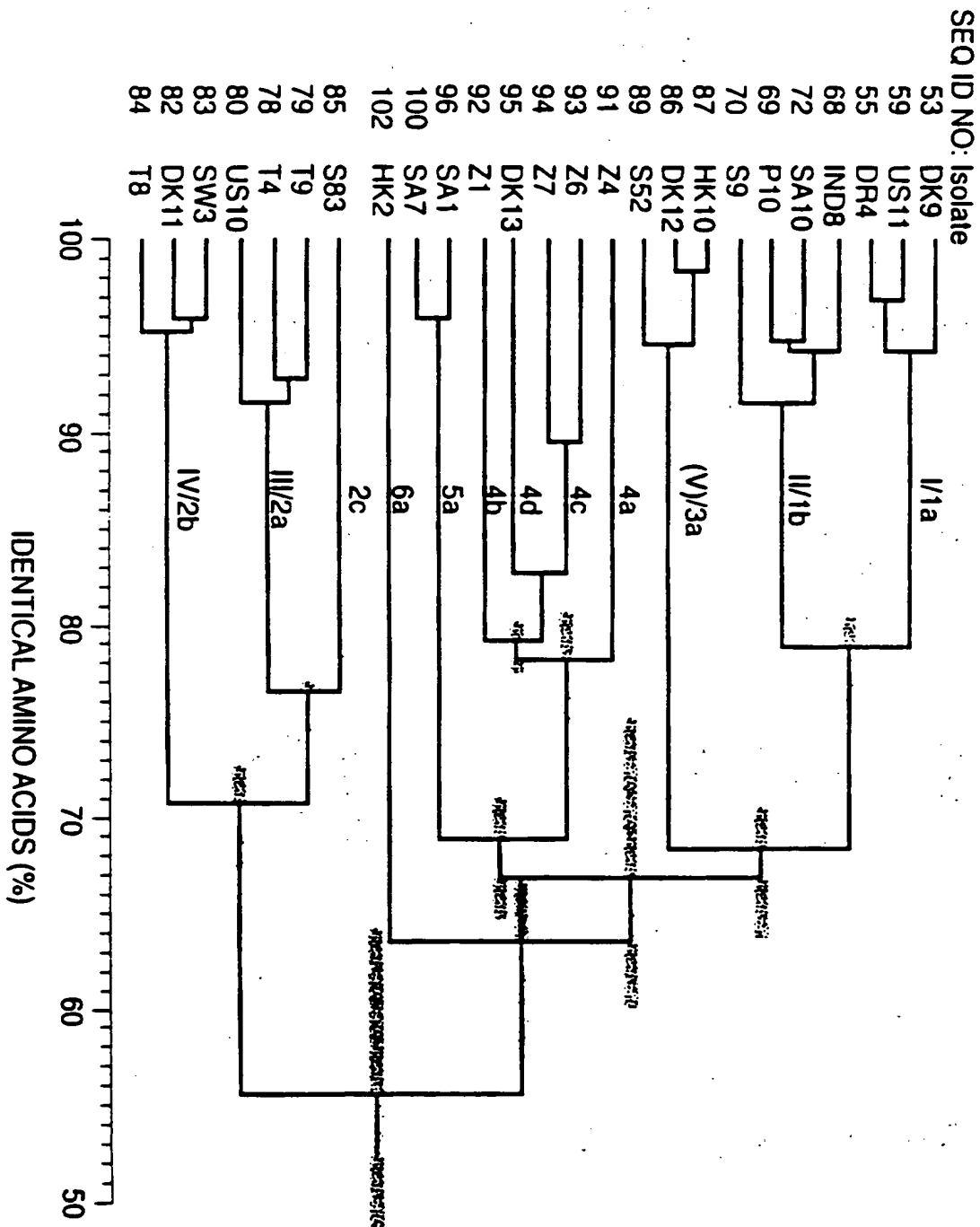
FIGURE 3A

Genotype	Seq ID No:	Isolate	200	210	220	230	240	250	260	270	280
1V/2b	82	DK11	yevrntsgv	hvt	IND	h	h	h	h	h	h
	83	SV3	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	81	DK8	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	84	T8	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
2c	85	SB3	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
111/2a	78	T4	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	80	US10	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	79	T9	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	77	T2	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
(V)/3a	86	DK12	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	87	HK10	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	88	S2	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	90	S54	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	89	S52	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
11/1b	68	IND8	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	67	IND5	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	73	SV2	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	63	DK3	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	66	HK8	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	71	S45	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	61	D3	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	74	T3	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	65	HK5	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	64	HK4	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	76	US6	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	69	P10	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	72	SA10	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	75	T10	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	62	DK1	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	70	S9	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	60	D1	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
1/1a	52	DK7	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	59	US11	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	55	DR4	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	54	DR1	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	53	DK9	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	58	SV1	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	56	S14	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	57	S18	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
4a	91	Z4	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
4c	93	Z6	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	94	Z7	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
4d	95	DK13	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
4b	92	Z1	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
5a	98	SA5	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	100	SA7	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	97	SA4	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	96	SA1	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	99	SA6	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
	101	SA13	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---
6a	102	HK2	VEVRNTSS	YA	---	S	-	IT	TL	NAVL	---

[illegible]

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FIG. 4



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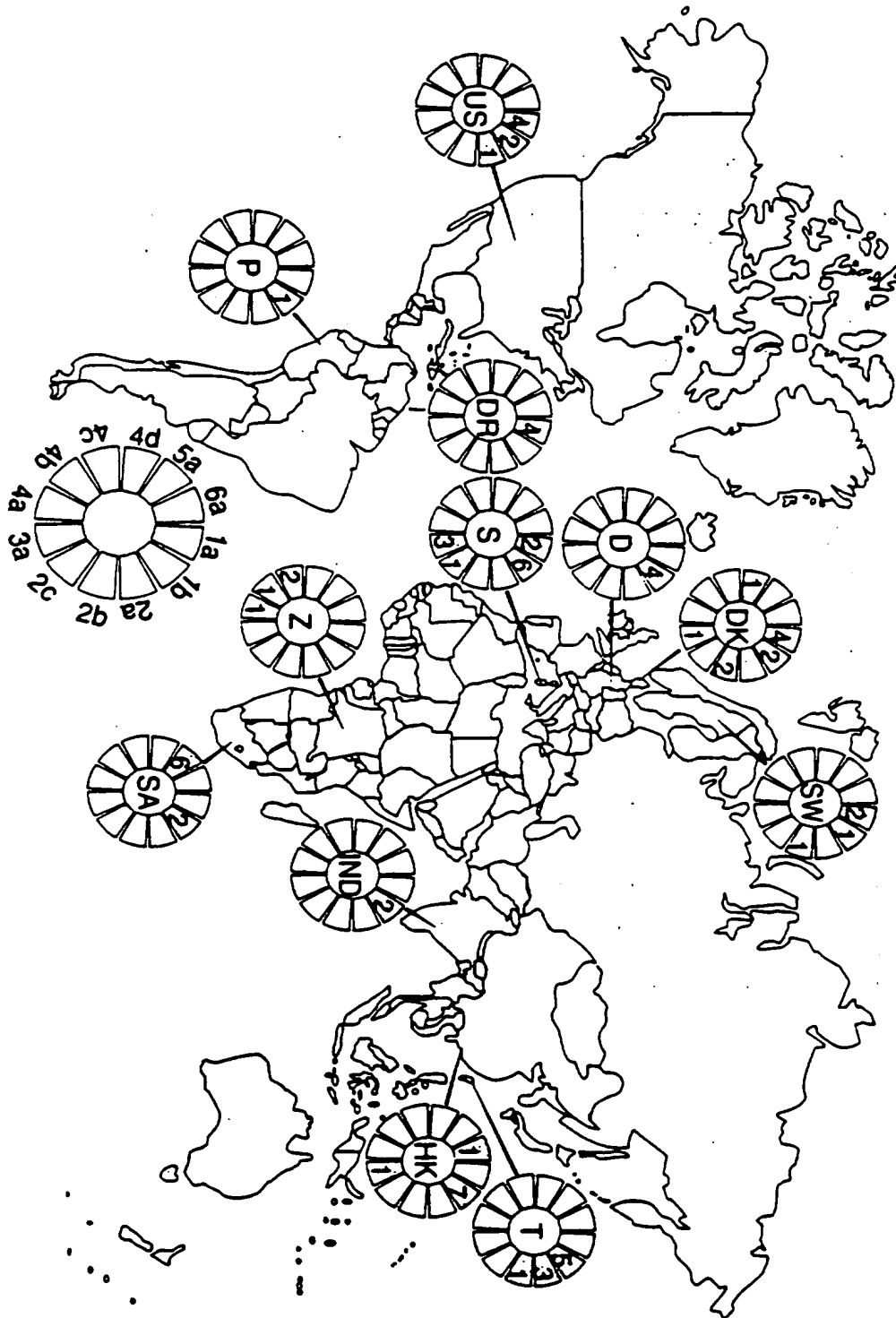


FIG. 5

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FIGURE 6A-1

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
108	DR4	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCCGTCGCCACACAGG
103	DK7	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCCGTCGCCACACAGG
104	US11	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCCGTCGCCACACAGG
105	S14	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCCGTCGCCACACAGG
106	SW1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCCGTCGCCACACAGG
107	S18	1 ATGAGCACaAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCCGTCGCCACACAGG
103-108	consensus	ATGAGCACgAATCCTAAACCTCAAAGAAAAACCAAAACGTAACACCAACCCGTCGCCACACAGG
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
108	DR4	62 ACGTCAAGTTCCCGGGTGGCGGTcAGATCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG
103	DK7	62 ACGTCAAGTTCCCGGGTGGCGGTcAGATCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG
104	US11	62 ACGTCAAGTTCCCGGGTGGCGGTcAGATCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG
105	S14	62 ACGTCAAGTTCCCGGGTGGCGGTcAGATCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG
106	SW1	62 ACGTCAAGTTCCCGGGTGGCGGTcAGATCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG
107	S18	62 ACGTtAAGTTCCCGGGTGGCGGTcAGATCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG
103-108	consensus	ACGTcAAGTTCCCGGGTGGCGGTcAGATCGTTGGTGGAGTTTACTTGTGCGCGCAGGGG
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
108	DR4	123 CCCTAGATTGGGTGTGCGCGGcGAGGAAGACTTCCGAGCGGTcGCAACCTCGAGGTAGA
103	DK7	123 CCCTAGATTGGGTGTGCGCGGcGAGGAAGACTTCCGAGCGGTcGCAACCTCGAGGTAGA
104	US11	123 CCCTAGATTGGGTGTGCGCGGcGAGGAAGACTTCCGAGCGGTcGCAACCTCGAGGTAGA
105	S14	123 CCCTAGATTGGGTGTGCGCGGcGAGGAAGACTTCCGAGCGGTcGCAACCTCGAGGTAGA
106	SW1	123 CCCTAGATTGGGTGTGCGCGGcGAGGAAGACTTCCGAGCGGTcGCAACCTCGAGGTAGA
107	S18	123 CCCTAGATTGGGTGTGCGCGGcGAGGAAGACTTCCGAGCGGTcGCAACCTCGcGGTAGA
103-108	consensus	CCCTAGATTGGGTGTGCGCGGcGAGGAAGACTTCCGAGCGGTcGCAACCTCGaGGTAGA

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FIGURE 6A-2

<u>SEQ ID NO:</u> 108	<u>ISOLATE</u> DR4	184	CGTCAGCCTATCCCCAAGGCGCTCGGCCCGAGGGCAGGACCTGGGGCTAGCCCCGGGTACC
103	DK7	184	CGTCAGCCTATCCCCAAGGCGCTCGGCCCGAGGGCAGGACCTGGGGCTAGCCCCGGGTACC
104	US11	184	CGTCAGCCTATCCCCAAGGCGCTCGGCCCGAGGGCAGGACCTGGGGCTAGCCCCGGGTACC
105	S14	184	CGTCAGCCTATCCCCAAGGCGCTCGGCCCGAGGGCAGGACCTGGGGCTAGCCCCGGGTATC
106	SW1	184	CGTCAGCCTATCCCCAAGGCGCTCGGCCCGAGGGCAGGACCTGGGGCTAGCCCCGGGTATC
107	S18	184	CGTCAGCCTATCCCCAAGGCGCTCGGCCCGAGGGCAGGACCTGGGGCTAGCCCCGGGTACC
103-108	consensus		CGTCAGCCTATCCCCAAGGC - CGTCGGCCCGAGGGCAGGACCTGGGGCTAGCCCCGGGTACC
<u>SEQ ID NO:</u> 108	<u>ISOLATE</u> DR4	245	CTTGGCCCCCTATGGCAATGAGGGCTGCGGGTGGCGGGATGGCTCCTGTCCCCCGTGG
103	DK7	245	CTTGGCCCCCTATGGCAATGAGGGCTGCGGGTGGCGGGATGGCTCCTGTCCCCCGTGG
104	US11	245	CTTGGCCCCCTATGGCAATGAGGGCTGCGGGTGGCGGGATGGCTCCTGTCCCCCGTGG
105	S14	245	CTTGGCCCCCTATGGCAATGAGGGCTGCGGGTGGCGGGATGGCTCCTGTCCCCCGTGG
106	SW1	245	CTTGGCCCCCTATGGCAATGAGGGCTGCGGaTGGCGGGATGGCTCCTGTCCCCCGTGG
107	S18	245	CTTGGCCCCCTATGGCAATGAGGGCTGCGGgTGGCGGGATGGCTCCTGTCCCCCGTGG
103-108	consensus		CTTGGCCCCCTATGGCAATGAGGGCTGCGGgTGGCGGGATGGCTCCTGTCC - CCCCCGTGG
<u>SEQ ID NO:</u> 108	<u>ISOLATE</u> DR4	306	CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCCGCGtAGTCCGCCAATTTGGTAAGTTC
103	DK7	306	CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCCGCGcAGTCCGCCAATTTGGTAAGTTC
104	US11	306	CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCCGCGTAGTCCGCCAATTTGGTAAGTTC
105	S14	306	CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCCGCGTAGTCCGCCAATTTGGTAAGTTC
106	SW1	306	CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCCGCGTAGTCCGCCAATTTGGTAAGTTC
107	S18	306	CTCCCGGCCTAGCTGGGGCCCCACAGACCCCCCGCGTAGTCCGCCAATTTGGGcAAAGTTC
103-108	consensus		CTCtCGGCCTAGCTGGGGCCCCcAcAGACCCCCCGCGtAGTCCGCCAATTTGGGtAAGTTC

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FIGURE 6A-3

SEQ ID NO:	ISOLATE	
108	DR4	367 ATCGACACCCTcACGTGGGCTTCGCCGACCTCATGGGGTACATcCCGCTCGTCGGCGCCCC
103	DK7	367 ATCGATACCCTTACGTGGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCC
104	US11	367 ATCGATACCCTTACGTGGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCC
105	S14	367 ATCGATACCCCTACGTGGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCC
106	SW1	367 ATCGATACCCCTACGTGGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCCC
107	S18	367 ATCGATACCCCTACGTGGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCCC
103-108	consensus	ATCGAtACCCTcACGTGGGCTTCGCCGACCTCATGGGGTACATaCCGCTCGTCGGCGCCCC
SEQ ID NO:	ISOLATE	
108	DR4	428 CcCTTGGgGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGaGTTCTGGAAGACGGCGTGAA
103	DK7	428 CTCTTGGAGGCGTGCCAGGGCCCTGGCGCATGGCGTCCGGTTCTGGAAGACGGCGTGAA
104	US11	428 CTCTGGAGGCGTGCCAGGGCCCTGGCGCATGGCGTCCGGTTCTGGAAGACGGCGTGAA
105	S14	428 CcCTGGgGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGTTCTGGAAGACGGCGTGAA
106	SW1	428 CTCTtGGAGGCGTGCCAGGGCCCTGGCGCATGGCGTCCGGTTCTGGAAGACGGCGTGAA
107	S18	428 CTCTcGGAGGCGTGCCAGGGCCCTGGCGCATGGCGTCCGGTTCTGGAAGACGGCGTGAA
103-108	consensus	CtCT-GGaGGCGTGCCAGGGCCCTGGCGCATGGCGTCCGgGTTCTGGAAGACGGCGTGAA
SEQ ID NO:	ISOLATE	
108	DR4	489 CTATGCAACAGGGAAtCTTCCGTGGTTGCTCTTTCTCTATCTTCCCTTTGGCcttTGCTCTCT
103	DK7	489 CTATGCAACAGGGAACCTTCCGTGGTTGCTCTTTCTCTATCTTCCCTTTGGCCCTGCTCTCT
104	US11	489 CTATGCAACAGGGAACCTTCCGTGGTTGCTCTTTCTCTATCTTCCCTTGTGCCCCCTGCTCTCT
105	S14	489 CTATGCAACAGGGAACCTTCCGTGGTTGCTCTTTCTCTATCTTCCCTTGTGCCCCCTGCTCTCT
106	SW1	489 CTATGCAACAGGGAACCTTCCGTGGTTGCTCTTTCTCTATCTTCCCTTGTGCCCCCTGCTTTCT
107	S18	489 CTATGCAACAGGGAACCTTCCGTGGTTGCTCTTTCTCTATCTTCCCTTGTGCCCCCTGCTcTCT
103-108	consensus	CTATGCAACAGGGAACcTTCCGTGGTTGCTCTTTCTCTATCTTCCCTtctgGccctTGCTcTCT

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FIGURE 6A-4

<u>SEQ ID NO:</u>	<u>ISOLATE</u>
108	DR4
103	DK7
104	US11
105	S14
106	SW1
107	S18
103-108	consensus

550	TGctTGACCGTGCCCCGCaTCGGCC
550	TGCCTGACCGTGCCCCGCTTCGGCC
550	TGCCTGACTGTGCCCCGCTTCAGCC
550	TGCCTGACTGTGCCCCGCTTCAGCC
550	TGCCTGACaGTGCCCCGCGTCAGCC
550	TGtCTGACTGTGCCCCGCGTCAGCt
	TGcctGACTGTGCCCCGCTTCaGcC

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FIGURE 6B-1

SEQ ID NO:	ISOLATE	
119	S9	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
117	IND3	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
118	IND8	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
111	D1	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
112	US6	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
113	P10	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
114	DK1	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
115	T10	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
116	SW2	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
122	HK4	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
109	SA10	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
110	S45	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
123	P8	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
124	T3	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
120	HK3	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
121	HK5	1 ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG
109-124	consensus	ATGAGCACGAATCCTTAAACCTCAAAGAAAAACCAAAACGTAAACCAACCGCGCGCCACAGG

SEQ ID NO:	ISOLATE
1119	S9
1117	IND3
1118	IND8
1111	D1
1112	US6
1113	P10
1114	DK1
1115	T10
1116	SW2
1122	HK4
1109	SA10
1110	S45
1123	P8
1124	T3
1120	HK3
1121	HK5
1109-124	consensus

FIGURE 6B-3

SEQ ID NO:	ISOLATE	
119	S9	123 CCCAGGTTGGGTGTGCGCGCaACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
117	IND3	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
118	IND8	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
111	D1	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
112	US6	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
113	P10	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
114	DK1	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
115	T10	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
116	SW2	123 CCCcGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
122	HK4	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
109	SA10	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
110	S45	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
123	P8	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
124	T3	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
120	HK3	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
121	HK5	123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCCGAGCGGTGCGAACCTCGTGGAAGG
109-124	consensus	CCCCaGGTTGGGTGTGCGCGGcGActAGGAAGACTTCCGAGCGGTcGcAACCTCGTGGAaGG

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FIGURE 6B-4

SEQ ID NO:	ISOLATE	
119	S9	184 CGACAACTATCCCCAAGGCTCGCCatCCCGAGGGcAGGGCTGGGCTAGCCCGGGTACC
117	IND3	184 CGACAACTATCCCCAAGGCTCGCCGGCCCCAGGGTAGGGCTGGGCTAGCCCGGGTACC
118	IND8	184 CGACAACTATCCCCAAGGCTCGCCGGCCCCAGGGTAGGGCTGGGCTAGCCCGGGTACC
111	D1	184 CGACAACTATCCCCAAGGCTCGCCGGCCCCAGGGTAGGGCTGGGCTAGCCCGGGTACC
112	US6	184 CGACAACTATCCCCAAGGCTCGCCGGCCCCAGGGTAGGGCTGGGCTAGCCCGGGTACC
113	P10	184 CGACAACTATCCCCAAGGCTCGCCGGCCCCAGGGTAGGGCTGGGCTAGCCCGGGTACC
114	DK1	184 CGACAACTATCCCCAAGGCTCGCCGGCCCCAGGGTAGGGCTGGGCTAGCCCGGGTACC
115	T10	184 CGACAgCCTATCCCCAAGGCTCGCCAGCCCCGAGGGCAGGGCTGGGCTAGCCCGGGTACC
116	SW2	184 CGACAACTATCCCCAAGGCTCGCCAGCCCCGAGGGCAGGGCTGGGCTAGCCCGGGTACC
122	HK4	184 CGACAACTATCCCCAAGGCTCGCCAGCCCCGAGGGCAGGGCTGGGCTAGCCCGGGTACC
109	SA10	184 CGACAACTATCCCCAAGGCTCGCCAGCCCCGAGGGCAGGGCTGGGCTAGCCCGGGTACC
110	S45	184 CGACAACTATCCCCAAGGCTCGCCGGCCCCGAGGGCAGGGCTGGGCTAGCCCGGGTACC
123	P8	184 CGACAACTATCCCCAAGGCTCGCCGGCCCCGAGGGTAGGGCTGGGCTAGCCCGGGTACC
124	T3	184 CGACAACTATCCCCAAGGCTCGCCGGCCCCGAGGGTAGGGCTGGGCTAGCCCGGGTACC
120	HK3	184 CGACAACTATCCCCAAGGCTCGCCaACCCGAGGGCAGGACCTGGGCTAGCCCGGGTATC
121	HK5	184 CGACAACTATCCCCAAGGCTCGCCgACCCGAGGGCAGGACCTGGGCTAGCCCGGGTATC
109-124	consensus	CGACAaCCTATCCCCAAGGCTCGCCggCCCGAGGGcAGGgCCTGGGCTAGCCCGGGTACC

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FIGURE 6B-5

SEQ ID NO:	ISOLATE	
119	S9	245 CTTGGCCCCCTCTACGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCCGtGG
117	IND3	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCCGCGG
118	IND8	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCCGCGG
111	D1	245 CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCCGCGG
112	US6	245 CTTGGCCCCCTCTATGGCAACGAGGGCaTGGGGTGGGCAGGATGGCTCCTGTCACCCCCGTGG
113	P10	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
114	DK1	245 CTTGGCCCCCTCTATGGCAATGAGGGCATGGGGTGGGCAGGATGGCTCCTGTCACCCCGcGG
115	T10	245 CTTGGCCCCCTCTATGGCAATGAGGGCATGGGGTGGGCAGGATGGCTCCTGTCACCCCCGtGG
116	SW2	245 CcTGGCCCCCTCTATGGCAATGAGGGCATGGGaTGGGCAGGATGGCTCCTGTcCCCCCGCGG
122	HK4	245 CTTGGCCCCCTCTATGGCAATGAGGGCATGGGGTGGGCAGGATGGCTCCTGTCACCCCCGCGG
109	SA10	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
110	S45	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
123	P8	245 CTTGGCCCCCTCTATGcCAATGAGGGCTTGGGGTGGGCgGGATGGCTCCTGTCACCCCCGCGG
124	T3	245 CTTGGCCCCCTCTATGGCgACGAGGGCATGGGGTGGGCAGGATGGCTCCTGTCACCCCCGCGG
120	HK3	245 CTTGGCCCCCTCTATGGCAACGAGGGCATGGGGTGGGCAGGATGGCTCCTGTCACCCCCGCGG
121	HK5	245 CTTGGCCCCCTCTATGGCAATGAGGGCATGGGGTGGGCAGGATGGCTCCTGTCACCCCCatGG
109-124	consensus	CtTGGCCCCCTCTAtGgCaAtGAGGGC - TGGGgTGGGCaGGATGGCTCCTGTCaCCCCGcGG

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FIGURE 6B-6

SEQ ID NO:	ISOLATE	
119	S9	306 cTCTCGGCCTAGTTGGGGCCCCCAatGACCCCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
117	IND3	306 tTCTCGGCCTAGTTGGGGCCCCCACAGACCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
118	IND8	306 CTCTCGGCCTAGTTGGGGCCCCCACAGACCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
111	D1	306 CTCCCGGCCTAGTTGGGGCCCCCACcGACCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
112	US6	306 CTCCCGGCCTAGTTGGGGCCCCCACGGACCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
113	P10	306 CTCTCGGCCTAGTTGGGGCCCCCACGGACCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
114	DK1	306 CTCTCGGCCTAGTTGGGGCCCCCAacGACCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
115	T10	306 CTCCCGGCCTAGTTGGGGCCCCCACaGACCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
116	SW2	306 CTCTCGGCCTAGTTGGGGCCCCCAcTgACCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
122	HK4	306 CTCTCGGCCTAGTTGGGGCCCCCACGGACCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
109	SA10	306 CTCTCGGCCTAGTTGGGGCCCCCACGGACCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
110	S45	306 CTCCCGGCCTAGTTGGGGCCCCCACGGACCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
123	P8	306 CTCCCGGCCTAGTTGGGGCCCCCACGGACCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
124	T3	306 CTCCCGGCCTAATTTGGGGCCCCCACaGACCCCGCGTAGGTCGCGTAATcTGGGTAAGGTC
120	HK3	306 CTCTCGGCCTAATTTGGGGCCCCCACGGACCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
121	HK5	306 CTCTCGGCCTAgTTGGGGCCCCCACGGACCCCGCGTAGGTCGCGTAATTTGGGTAAGGTC
109-124	consensus	cTctCGGCCTAGTTGGGGCCCCCAcgGACCCCGCGTAGGTCGCGTAATtTGGGTAAGGTC

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FIGURE 6B-7

SEQ ID NO:	ISOLATE	
119	S9	367 ATCGATACCCCTCACATGCGGCTTtGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
117	IND3	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATcCCGCTCGTCGGCGCCC
118	IND8	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATcCCGCTCGTCGGCGCCC
111	D1	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATcCCGCTCGTCGGCGCCC
112	US6	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
113	P10	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
114	DK1	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
115	T10	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
116	SW2	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
122	HK4	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
109	SA10	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
110	S45	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
123	P8	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGCCC
124	T3	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATtCCGCTCGTCGGCGGcC
120	HK3	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATcCCGCTCGTCGGtGCCC
121	HK5	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGCGGTACATcCCGCTCGTCGGcGCCC
109-124	consensus	ATCGATACCCCTCACaTGCGGCTTcGCCGACCTCATGCGGTACATtCCGCTCGTCGGcGccc

FIGURE 6B-8

SEQ ID NO:	ISOLATE	
119	S9	428 CCTAGGGGGCGCTGCCAGGGCtCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
117	IND3	428 CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTcCTGGAGGACGGCGTGAA
118	IND8	428 CCTAGGGGGTGTCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTcCTGGAGGACGGCGTGAA
111	D1	428 CCTAGGGGGTGTCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
112	US6	428 CCTAGGGGGCGCTGCCAGGGCCtTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
113	P10	428 CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
114	DK1	428 CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
115	T10	428 CCTAGGGGGCGCTGCCAGGGCtCTGGCaCATGGtGTCCGGGTtCTGGAGGACGGCGTGAA
116	SW2	428 CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGcGTCCGGGTcCTGGAGGACGGCGTGAA
122	HK4	428 CCTAGGGGGCGtTGCCAGaGCCCCTGGCaCATGGtGTCCGGGTgTGGAGGACGGCGTGAA
109	SA10	428 CtTTAGGGGGCGCTGCCAGgCCCTTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
110	S45	428 CCTAGGGGGCGCTGCCAGaGCCCTTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
123	P8	428 CCTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTgTGGAGGACGGCGTGAA
124	T3	428 CctTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTtCTGGAGGACGGCGTGAA
120	HK3	428 CCTAGGGGGCGTTGCCAGAGCCtTGGACATGGTGTCCGGGTtCTGGAGGACGGCGTGAA
121	HK5	428 CCTAGGGGGCGTTGCCAGAGCCcTGGACACACGGTGTCCGGGTtCTGGAGGACGGCGTGAA
109-124	consensus	CccTAGGGGGcGcTGCCAGgGccTGGCGcATGGcGTCCGGGTtCTGGAGGACGGCGTGAA

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FIGURE 6B-9

SEQ ID NO:	ISOLATE	
119	S9	489 CTATGCAACAGGGAAcTcCCCCGGTTGCTCTTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
117	IND3	489 CTATGCAACAGGGAAcTTGCCCGGTTGCTCTTTTCTCTATCTTCCCTTTAgCTTTGCTATCC
118	IND8	489 CTATGCAACAGGGAAcTTGCCCGGTTGCTCTTTTCTCTATCTTCCCTTTGGCTTTGCTATCC
111	D1	489 tTATGCAACAGGGAAcTTGCCCGGTTGCTCTTTTCTCTATCTTCCCTTTGGCTTTGCTGTCC
112	US6	489 CTATGCAACAGGGAAcTTGCCCGGTTGCTCTTTTCTCTATCTTCCCTTTGGCTTTGCTGTCC
113	P10	489 CTATGCAACAGGGAAcTTGCCCGGTTGCTCTTTTCTCTATCTTCCCTTTGGCTTTGCTGTCC
114	DK1	489 CTAcGCAACAGGGAAcTTGCCCGGTTGCTCTTTTCTCTATCTTCCCTTTGGCTTTGCTGTCC
115	T10	489 CTATGCAACAGGGAAcTTGCCCGGTTGCTCTTTTCTCTATCTTCCCTTTGGCTTTGCTGTCC
116	SW2	489 CTATGCAACAGGGAAcTTGCCCGGTTGCTCTTTTCTCTATCTTCCCTTTGGCTTTGCTGTCC
122	HK4	489 CTATGCAACAGGGAAcTTGCCCGGTTGCTCTTTTCTCTATCTTCCCTTTGGCTTTGCTGTCC
109	SA10	489 CTATGCAACAGGGAAcTTGCCCGGTTGCTCTTTTCTCTATCTTCCCTTTGGCTTTGCTGTCC
110	S45	489 CTATGCAACAGGGAAcTTGCCCGGTTGCTCTTTTCTCTATCTTCCCTTTGGCTTTGCTGTCC
123	P8	489 CTATGCAACAGGGAAcTTGCCCGGTTGCTCTTTTCTCTATCTTCCCTTTGGCTTTGCTGTCC
124	T3	489 tTAcGCAACAGGGAAcTTGCCCGGTTGCTCTTTTCTCTATCTTCCCTTTGGCTTTGCTGTCC
120	HK3	489 CTAtGCAACAGGGAAcTTAcCCCGGTTGCTCTTTTCTCTATCTTCCCTTTGGCTTTGCTGTCC
121	HK5	489 CTAcGCAACAGGGAAcTaACCCCGGTTGCTCTTTTCTCTATCTTCCCTTTGGCTTTGCTGTCC
109 - 124	consensus	cTAtGCAACAGGGAAcTtTgCCcGGTTGCTcTtTcTCTATcTTCCtTcTgGCTtTgCtTgTCC

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FIGURE 6B-10

119	SEQ ID NO:	ISOLATE	550	TGTTTGACCATCCAGCTTCCGCT
117		S9	550	TGTTTGACCATCCAGCTTCCGCT
118		IND3	550	TGTTTGACCATCCAGCTTCCGCT
111		IND8	550	TGTTTGACCATCCAGCTTCCGCT
112		D1	550	TGTTTGACCATCCAGCTTCCGCT
113		US6	550	TGTTTGACCATCCAGCTTCCGCT
114		P10	550	TGcCTGACCATCCAGCGTCCGCT
115		DK1	550	TGTTTGACCATCCAGCTTCCGCT
116		T10	550	TGTTTGACCATCCAGCTTCCGCT
122		SW2	550	TGTTTGACCATCCAGCTTCCGCT
109		HK4	550	TGTTTGACCATCCAGCTTCCGCT
110		SA10	550	TGTTTaACCATCCAGCTTCCGCT
123		S45	550	TGcTTGACCATCCAGCTTCCGCT
124		P8	550	TGcCTGACCATCCAGCTTCCGCT
120		T3	550	TGCTTGACCATCCAGCTTCCGCT
121		HK3	550	TGCTTGACCATCCAGCTTCCGCT
		HK5	550	TGtCTGACCATCCAGCTTCCGCT
109-124		consensus		TGtTTgACCATcCCAGctTCCGct

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FIGURE 6C-1

SEQ ID NO:	ISOLATE	
119	S9	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
117	IND3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
118	IND8	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
111	D1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
112	US6	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
113	P10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
114	DK1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
115	T10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
116	SW2	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
122	HK4	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
109	SA10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
110	S45	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
123	P8	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
124	T3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
120	HK3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
121	HK5	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
108	DR4	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
104	US11	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
105	S14	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
106	SW1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
107	S18	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
103	DK7	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG
103-124	consensus	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAACCGTAACACCAACCGCGCCACAGG

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FIGURE 6C-2

SEQ ID NO:	ISOLATE	
119	S9	62 ACGTtAAGTtCCCGGGCGGTGGtCAGATCGTcGGTGGAGTtTACCTGTtGCCGCGCAGGGG
117	IND3	62 ACGTCAAGTtCCCGGGCGGTGGCCAGATCGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
118	IND8	62 ACGTCAAGTtCCCGGGCGGTGGCCAGATCGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
111	D1	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
112	US6	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
113	P10	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
114	DK1	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
115	T10	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
116	SW2	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
122	HK4	62 ACGTtAAGTtCCCGGGCGGTGGCCAGATCGTcGGTGGAGTtTACCTGTtGCCGCGCAGGGG
109	SA10	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
110	S45	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
123	P8	62 ACGTtAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
124	T3	62 ACGTtAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
120	HK3	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
121	HK5	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
108	DR4	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
104	US11	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
105	S14	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
106	SW1	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
107	S18	62 ACGTtAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
103	DK7	62 ACGTCAAGTtCCCGGGCGGTGGTCAAGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG
103-124	consensus	ACGTcAAGTtCCCGGGcGGtGGtCAGATCGTtGGTGGAGTtTACCTGTtGCCGCGCAGGGG

FIGURE 6C-3

SEQ ID NO:	ISOLATE	
119	S9	123 CCCAGGTTGGGTGTGCGCGCaACTAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
117	IND3	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
118	IND8	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
111	D1	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
112	US6	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
113	P10	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
114	DK1	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
115	T10	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
116	SW2	123 CCCcGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
122	HK4	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
109	SA10	123 CCCAGGTTGGGTGTGCGCGCGACgAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
110	S45	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
123	P8	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
124	T3	123 CCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
120	HK3	123 CCCAGGTTGGGTGTGCGCGCGACCAGGAAGACTTcAGAGCGGTGCGAACTTCGTGGAAGG
121	HK5	123 CCCAGGTTGGGTGTGCGCGCGACCAGGAAGACTTCCGAGCGGTGCGAACTTCGTGGAAGG
108	DR4	123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGAACTTCGAGGTAGA
104	US11	123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGAACTTCGAGGTAGA
105	S14	123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGAACTTCGAGGTAGA
106	SW1	123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGAACTTCGAGGTAGA
107	S18	123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGAACTTCGcGGTAGA
103	DK7	123 CCCTAGATTGGGTGTGCGCGCGcCGAGGAAGACTTCCGAGCGGTGCGAACTTCGAGGTAGA
103-124	consensus	CCCcaGgTTGGGTGTGCGCGCGaCtAGGAAGACTTCCGAGCGGTcGcAACTTCGTGGAaGg

FIGURE 6C-4

SEQ ID NO:	ISOLATE	
119	S9	184 CGACAACTATCCCCAAGGCTCGCCatCCCCAGGGcAGGGCTGGGCTCAGCCCGGGTACC
117	IND3	184 CGACAACTATCCCCAAGGCTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
118	IND8	184 CGACAACTATCCCCAAGGCTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
111	D1	184 CGACAACTATCCCCAAGGCTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
112	US6	184 CGACAACTATCCCCAAGGCTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
113	P10	184 CGACAACTATCCCCAAGGCTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
114	DK1	184 CGACAACTATCCCCAAGGCTCGCGGCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
115	T10	184 CGACAgCCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGGCTGGGCTCAGCCCGGGTACC
116	SW2	184 CGACAACTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGGCTGGGCTCAGCCCGGGTACC
122	HK4	184 CGACAACTATCCCCAAGGCTCGCCaCCCCAGGGCAGGACCTGGGCTCAGCCCGGGTACC
109	SA10	184 CGACAACTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
110	S45	184 CGACAACTATCCCCAAGGCTCGCCGGCCCCGAGGGCAGGGCTGGGCTCAGCCCGGGTACC
123	P8	184 CGACAACTATCCCCAAGGCTCGCCGGCCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
124	T3	184 CGACAACTATCCCCAAGGCTCGCCGGCCCCGAGGGTAGGGCTGGGCTCAGCCCGGGTACC
120	HK3	184 CGACAACTATCCCCAAGGCTCGCCaACCCAGGGCAGGACCTGGGCTCAGCCCGGGTACC
121	HK5	184 CGACAACTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
108	DR4	184 CGTCAGCCTATCCCCAAGGCTCGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
104	US11	184 CGTCAGCCTATCCCCAAGGCTCGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
105	S14	184 CGTCAGCCTATCCCCAAGGCTCGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
106	SW1	184 CGTCAGCCTATCCCCAAGGCTCGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
107	S18	184 CGTCAGCCTATCCCCAAGGCTCGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
103	DK7	184 CGTCAGCCTATCCCCAAGGCTCGTCGGCCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
103-124	consensus	CGACAACTATCCCCAAGGCTCGcCgCCCCGAGGGcAGGgCCTGGGCTCAGCCcGGGtAcC

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FIGURE 6C-5

SEQ ID NO:	ISOLATE	
119	S9	245 CTTGGCCCCCTCTACGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTCACCCCCGtGG
117	IND3	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTCACCCCCGGG
118	IND8	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTCACCCCCGGG
111	D1	245 CTTGGCCCCCTCTATGGCAACGAGGGCTTGGGGTGGGAGGATGGCTCCTGTCACCCCCGGG
112	US6	245 CTTGGCCCCCTCTATGGCAACGAGGGCaTGGGGTGGGAGGATGGCTCCTGTCACCCCCGTGG
113	P10	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTCACCCCGTGG
114	DK1	245 CTTGGCCCCCTCTATGGCAATGAGGGCATGGGGTGGGAGGATGGCTCCTGTCACCCCGGGG
115	T10	245 CTTGGCCCCCTCTATGGCAATGAGGGCATGGGGTGGGAGGATGGCTCCTGTCACCCCGGGG
116	SW2	245 CTTGGCCCCCTCTATGGCAATGAGGGCATGGGGTGGGAGGATGGCTCCTGTCACCCCGGGG
122	HK4	245 CTTGGCCCCCTCTATGGCAATGAGGGCATGGGGTGGGAGGATGGCTCCTGTCACCCCGGGG
109	SA10	245 CTTGGCCCCCTCTATGGCAATGAGGGCATGGGGTGGGAGGATGGCTCCTGTCACCCCGGGG
110	S45	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTCACCCCGTGG
123	P8	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTCACCCCGTGG
124	T3	245 CTTGGCCCCCTCTATGGCAATGAGGGCTTGGGGTGGGAGGATGGCTCCTGTCACCCCGGGG
120	HK3	245 CTTGGCCCCCTCTATGGCAACGAGGGCATGGGGTGGGAGGATGGCTCCTGTCACCCCGGGG
121	HK5	245 CTTGGCCCCCTCTATGGCAACGAGGGCATGGGGTGGGAGGATGGCTCCTGTCACCCCGGGG
108	DR4	245 CTTGGCCCCCTCTATGGCAATGAGGGCATGGGGTGGGAGGATGGCTCCTGTCACCCCaTGG
104	US11	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGAGGATGGCTCCTGTCACCCCGTGG
105	S14	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGAGGATGGCTCCTGTCACCCCGTGG
106	SW1	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGgaTGGGAGGATGGCTCCTGTCACCCCGTGG
107	S18	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGAGGATGGCTCCTGTCACCCCGTGG
103	DK7	245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGAGGATGGCTCCTGTCACCCCGTGG
103-124	consensus	CtTGGCCCCCTCTAtGgCaAtGAGGGCtTgGGgTGGGCaGGATGGCTCCTGTCACCCCgtGG

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FIGURE 6C-6

SEQ ID NO:	ISOLATE	
119	S9	306 cTCTCGGCCTAGTTGGGGCCCCAatGACCCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
117	IND3	306 tTCTCGGCCTAGTTGGGGCCCCACAGACCCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
118	IND8	306 CTCTCGGCCTAGTTGGGGCCCCACAGACCCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
111	D1	306 CTCCCGGCCTAGTTGGGGCCCCACcGACCCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
112	US6	306 CTCCCGGCCTAGTTGGGGCCCCACAGGACCCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
113	P10	306 CTCTCGGCCTAGTTGGGGCCCCACAGGACCCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
114	DK1	306 CTCTCGGCCTAGTTGGGGCCCCAacGACCCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
115	T10	306 CTCCCGGCCTAGTTGGGGCCCCACaGACCCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
116	SW2	306 CTCTCGGCCTAGTTGGGGCCCCACtGACCCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
122	HK4	306 CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCCGGCGTAGGTCGCGcAATTTGGGTAAGGTC
109	SA10	306 CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCCGGCGTAGGTCGCGtAATTTGGGTAAGGTC
110	S45	306 CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
123	P8	306 CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
124	T3	306 CTCCCGGCCTAATTGGGGCCCCACaGACCCCCCGGCGTAGGTCGCGtAATcTGGGTAAGGTC
120	HK3	306 CTCTCGGCCTAATTGGGGCCCCACGGACCCCCCGGCGTAGGTCGCGcAATTTGGGTAAGGTC
121	HK5	306 CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCCGGCGTAGGTCGCGtAATTTGGGTAAGGTC
108	DR4	306 CTCTCGGCCTAGTTGGGGCCCCACaGACCCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
104	US11	306 CTCTCGGCCTAGCTGGGGCCCCACgGACCCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
105	S14	306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
106	SW1	306 CTCTCGGCCTAGCTGGGGCCCCTACAGACCCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
107	S18	306 CTCCCGGCCTAGCTGGGGCCCCTACAGACCCCCCGGCGTAGGTCGCGCAATTTGGGcAAAGTC
103	DK7	306 CTctCGGCCTAGCTGGGGCCCCcACAGACCCCCCGGCGcAGGTCGCGCAATTTGGGtAAAGTC
103-124	consensus	cTctCGGCCTAgTtGGGGCCCCAc - GACCCCCCGGCGtAGGTCGCGtAATtTGGGtAAAGGTC

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FIGURE 6C-7

SEQ ID NO:	ISOLATE	
119	S9	367 ATCGATACCCCTCACATGGGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGGCCC
117	IND3	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
118	IND8	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
111	D1	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
112	US6	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
113	P10	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
114	DK1	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
115	T10	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
116	SW2	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
122	HK4	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
109	SA10	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
110	S45	367 ATCGATACCCCTCACgTGCGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
123	P8	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
124	T3	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
120	HK3	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
121	HK5	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
108	DR4	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
104	US11	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
105	S14	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
106	SW1	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
107	S18	367 ATCGATACCCCTCACATGGGGCTTcGCCGACCTCATGGGGTACATCCCCGCTCGTCGGCGGCCC
103	DK7	367 ATCGATACCCCTtACGTGCGGGCTTcGCCGACCTCATGGGGTACATaCCGCTCGTCGGCGGCCC
103-124	consensus	ATCGAtACCCCTcACaTGCGGGCTTcGCCGACCTCATGGGGTACATtCCGCTCGTCGGcGccc

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FIGURE 6C-8

SEQ ID NO:	ISOLATE	
119	S9	428 CCTAGGGGGCGCTGCCAGGGCCTCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
117	IND3	428 CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
118	IND8	428 CCTAGGGGGTGTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
111	D1	428 CCTAGGGGGTGTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
112	US6	428 CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
113	P10	428 CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
114	DK1	428 CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
115	T10	428 CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
116	SW2	428 CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
122	HK4	428 CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
109	SA10	428 CtTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
110	S45	428 CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
123	P8	428 CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
124	T3	428 CctTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
120	HK3	428 CCTAGGGGGCGCTGCCAGAGCCCTGGCACATGGTGTCCGGGTCTTGAGGACGGCGTGAA
121	HK5	428 CCTAGGGGGCGCTGCCAGAGCCCTGGCACATGGTGTCCGGGTCTTGAGGACGGCGTGAA
108	DR4	428 CCTAGGGGGCGCTGCCAGAGCCCTGGCACATGGTGTCCGGGTCTTGAGGACGGCGTGAA
104	US11	428 CCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
105	S14	428 CtTCGGaGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
106	SW1	428 CcTCGGgGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
107	S18	428 CTCTtGGAGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
103	DK7	428 CTCTtGGAGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCTTGAGGACGGCGTGAA
103-124	consensus	CccTaGGgGGcGcTGCCAGgGCCcTGCGcGcCaTGGcGTCCGGgGtTcTGGAgGACGGCGTGAA

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FIGURE 6C-9

SEQ ID NO:	ISOLATE	
119	S9	489 CTATGCAACAGGGAACcTcCCCGGTTGCTCTTTCTCTATCTTCCCTTcTgGCTTTGCTgTCC
117	IND3	489 CTATGCAACAGGGAACcTtGCCCCGGTTGCTCTTTCTCTATCTTCCCTTTaGCTTTGCTATCC
118	IND8	489 CTATGCAACAGGGAACcTtGCCCCGGTTGCTCTTTCTCTATCTTCCCTTTTGGCTTTGCTATCC
111	D1	489 tTATGCAACAGGGAAtTTGCCCGGTTGCTCTTTCTCTATCTTCCCTCTTGGCTTTGCTGTCC
112	US6	489 CTATGCAACAGGGAACcTtGCCCCGGTTGCTCTTTCTCTATCTTCCCTCTTGGCTTTGCTGTCC
113	P10	489 CTATGCAACAGGGAAtcTGCCCCGGTTGCTCTTTCTCTATCTTCCCTCTTGGCTTTGCTGTCC
114	DK1	489 CTACGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCCTCTTGGCTCTGtTGTC
115	T10	489 CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCCTCTTGGCTCTGCTGTcT
116	SW2	489 CTATGCAACAGGGAATcTGCCCCGGTTGCTcTtTTTCTATCTTCCCTCTTGGCTcTGCTGTCC
122	HK4	489 CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCCTCTTGGCTcTGCTGTCC
109	SA10	489 CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCCTCTTGGCTcTGCTGTCC
110	S45	489 CTATGCAACAGGGAATcTGCCCCGGTTGCTcTtTTCTCTATCTTCCCTCTTGGCTcTGCTGTCC
123	P8	489 CTATGCAACAGGGAATcTGCCCCGGTTGCTCTTTCTCTATCTTCCCTCTTGGCTcTGCTGTcT
124	T3	489 tTAcGCAACAGGGAATTTGCCCTGGTTGCTCTTTCTCTATCTTCCCTCTTGGCTTTGCTGTCC
120	HK3	489 CTAtGCAACAGGGAATtTAcCCGGTTGCTCTTTCTCTATCTTCCCTCTTGGCTTTGCTGTCC
121	HK5	489 CTAcGCAACAGGGAATaTAcCCGGTTGCTCTTTCTCTATCTTCCCTCTTGGCTTTGCTGTCC
108	DR4	489 CTATGCAACAGGGAATcTtCCCTGGTTGCTCTTTCTCTATCTTCCCTCTTGGCTTTGCTCTCT
104	US11	489 CTATGCAACAGGGAACcTtCCCTGGTTGCTCTTTCTCTATCTTCCCTCTTGGCCCTGCTCTCT
105	S14	489 CTATGCAACAGGGAACcTtCCCTGGTTGCTCTTTCTCTATCTTCCCTcCTaGCCCCTGTCTTCT
106	SW1	489 CTATGCAACAGGGAACcTtCCCTGGTTGCTCTTTCTCTATCTTCCCTCTTGGCCCCTGTCTTCT
107	S18	489 CTATGCAACAGGGAACcTtCCCTGGTTGCTCTTTCTCTATCTTCCCTCTTGGCCCCTGTCTCTCT
103	DK7	489 CTATGCAACAGGGAACcTtCCCTGGTTGCTCTTTCTCTATCTTCCCTTtTGGCCCCTGTCTCTCT
103-124	consensus	cTAtGCAACAGGGAAtcTgCCcGGTTGCTcTtTcTCTATCTTCCCTcTtTgGCTtTGcTgTCC

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FIGURE 6C-10

SEQ ID NO:	ISOLATE	
119	S9	550 TGT TTG ACC ATCC CAG CTTC CGCT
117	IND3	550 TGT TTG ACC ATCC CAG CTTC CGCT
118	IND8	550 TGT TTG ACC G TCC CAG CTTC CGCT
111	D1	550 TGT TTG ACC ATCC CAG CTTC CGCT
112	US6	550 TGT TTG ACC ATCC CAG CTTC CGCT
113	P10	550 TG cc TG ACC ATCC CAG Cg TCC GCT
114	DK1	550 TGT t TG ACC ATCC CAG CTTC CGCc
115	T10	550 TGT CTG ACC ATCC CAG CTTC CGCT
116	SW2	550 TGT CTG ACC ATCC CAG CTTC CGCT
122	HK4	550 TGT TTG ACC ATCC CAG CTTC CGCT
109	SA10	550 TGT TTa ACC ATCC CAG CTTC CGCT
110	S45	550 TG c TTG ACC ATCC CAG CTTC CGCT
123	P8	550 TG c tTG ACC ATCC CAG CTTC CGCT
124	T3	550 TG CT TG ACC ATCC CAG CTTC CGCT
120	HK3	550 TG CT TG ACC ACC C CAG CTTC CGCT
121	HK5	550 TG t c TG ACC ACC C CAG t TC CGCT
108	DR4	550 TG Ct TG ACC GTG C CCG Ca TCg GCC
104	US11	550 TGC CTG ACT GTG C CCG CTTC AGCC
105	S14	550 TGC CTG ACT GTG C CCG CTTC AGCC
106	SW1	550 TGC CTG ACa GTG C CCG CCG TC AGCC
107	S18	550 TG t CTG ACT GTG C CCG CCG TC AGCT
103	DK7	550 TG c CTG AC c GTG C CCG CCG TCg GCC
103-124	consensus	TG t tTg AC c at c CCa G c t TC c G Ct

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FIGURE 6D-1

SEQ ID NO:	ISOLATE	
128	T2	1 ATGAGCACAAATCCTTAAACCTCAAAGAAAAACCAAAAGAAACACtAACCGTCGCCCCACAaG
125	T4	1 ATGAGCACAAATCCTTAAACCTCAAAGAAAAACCAAAAGAAACACcAACCGTCGCCCCACAaG
126	US10	1 ATGAGCACAAATCCTTAAACCTCAAAGAAAAACCAAAAGAAACACtAACCGTCGCCCCACAaG
127	T9	1 ATGAGCACAAATCCaAAACCCCAAAGAAAAACCCAtAAGAAACACcAACCGTCGCCCCACAaG
125-128	consensus	ATGAGCACAAATCCTTAAACCTCAAAGAAAAACCAaAAGAAACAC - AACCGTCGCCCCACA - G
SEQ ID NO:	ISOLATE	
128	T2	62 ACGTTAAGTTtCCGGCGGGCGGCCAGATCGTTGGCGGAGTATACTTgCTGCCCGCAGGGG
125	T4	62 ACGTTAAGTTtCCGGCGGGCGGCCAGATCGTTGGCGGAGTATACTTgTTGCCCGCAGGGG
126	US10	62 ACGTTAAGTTtCCGGCGGGCGGCCAGATCGTTGGCGGAGTATACTTgTTGCCCGCAGGGG
127	T9	62 ACGTTAAGTTtCCGGCGGGCGGCCAGATCGTTGGCGGAGTATACTTgTTGCCCGCAGGGG
125-128	consensus	ACGTTAAGTT - CCGGGCGGGCGGCCAGATCGTTGGCGGAGTATACTTgCTGCCCGCAGGGG
SEQ ID NO:	ISOLATE	
128	T2	123 CCCCAGGTTGGGTGTGCGCGCGACAAAGGAAGACTTCGGAGCGgTCCCAGCctCGTGGAAGG
125	T4	123 CCCCAGGTTGGGTGTGCGCGCGACAAAGGAAGACTTCGGAGCGaTCCCAGCCACGTGGGAGG
126	US10	123 CCCCAGGTTGGGTGTGCGCGCGACAAAGGAAGACTTCGGAGCGGTCCCAGCCACGTGGGAGG
127	T9	123 CCctAGGTTGGGTGTGCGCaCGACAAGGAAGACTTCGGAGCGGTCCCAGCCACGTGGGAGG
125-128	consensus	CCCcAGGTTGGGTGTGCGCgCGACAAGGAAGACTTCGGAGCGgTCCCAGCCaCGTGGgAGG
SEQ ID NO:	ISOLATE	
128	T2	184 CGCCAGCCCCATCCctAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAaAACcCAGGATAcC
125	T4	184 CGCCAGCCCCATCCCCAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAaAACcCAGGATAcC
126	US10	184 CGCCAGCCCCATCCCCAAAGATCGGCGCcCCACTGGCAAGTCCTGGGGAaAACcCAGGATAcC
127	T9	184 CGCCAGCCCCATCCCCAAAGATCGGCGctCCACTGGCAAGTCCTGGGGAaAACcCAGGATAcC
125-128	consensus	CGCCAGCCCCATCCCCAAAGATCGGCGctCCACTGGCAAGTCCTGGGGAaAACcCAGGATAcC

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FIGURE 6D-2

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	245 CCTGGCCCCCTGTATGGGAATGAGGGGCTCGGCTGGGCAGGATGGCTCCTGTCCCCCGGAGG
125	T4	245 CCTGGCCCCCTGTATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGGAGG
126	US10	245 CtTGGCCCCCTATATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGGAGG
127	T9	245 CcTGGCCCTCTATATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGGAGG
125-128	consensus	CcTGGCCcCT-TATGGGAATGAGGGaCTCGGCTGGGCaGGATGGCTCCTGTCCCCCGGAGG
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	306 TTCTCGTCCCTCTtTGGGGCCCCAATGACCCCCCGGCATAGGTCGGCAAtGTGGTAAGTC
125	T4	306 TTCCCGTCCCTCcTGGGGCCCCAATGACCCCCCGGCATAGGTCGGCAACGTGGTAAGTC
126	US10	306 TTCCCGTCCCTCTTGGGGCCCCCAATGATCCCCCGGCATAGGTCGGCAACGTGGTAAGTC
127	T9	306 TTCCCGTCCCTCTTGGGGCCCCCAATGAcCCCCCGGCATAGGTCGGCAACGTGGTAAGTC
125-128	consensus	TTCcCGTCCCTCTtTGGGGCCCCCAaTGAcCCCCCGGCATAGGTCGGCAAcGTGGTAAGTC
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	367 ATCGATACCCCTAACGTGCGGcTtTGCCGACCTCATGGGGTACaTCCCCGTCGTAGGCGcCC
125	T4	367 ATCGATACCCCTAACGTGCaGcTtTGCCGACCTCATGGGGTACgTCCCCGTCGTAGGCGGCC
126	US10	367 ATCGATACCCCTAACGTGCGGCTtTGCCGACCTCATGGGaTACATCCCCGTCGTgGGCGCtC
127	T9	367 ATCGATACCCCTAACGTGCGGCTtTGCCGACCTCATGGGgTACATCCCCGTCGTaGGCGCcc
125-128	consensus	ATCGATACCCCTAACGTGCGGcTtTGCCGACCTCATGGGgTACaTCCCCGTCGTaGGCGcCC
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	428 CGCtTGGTGGtGTCGCCAGAGCTCTtGCGCATGGCGTGAGAGTCCTGGAGGACGGaGTTAA
125	T4	428 CGtTgGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA
126	US10	428 CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGgGTCTGGAGGACGGGGTTAA
127	T9	428 CGCTTGGTGGCGTtGCCAGAGCTCTCGCGCAcGGCGTGAGaGTCTCTGGAGGACGGGGTTAA
125-128	consensus	CGCtTGGTGGcGTcGCCAGAGCTCTcGGCAtGGCGTGAGaGTCTCTGGAGGACGGgGTTAA

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FIGURE 6D-3

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	489 TTATGCAACAGGtAACTTACCcGGTTGCTCCTTTTCTATcTTCTTGCTaGCCCtgcTGTCc
125	T4	489 TTATGCAACAGGAACTTACCtGGTTGCTCCTTTTCTATtTTCTTGCTGGCCcTACTGTCC
126	US10	489 TTATGCAACAGGAACTTACCcGGTTGCTCCTTTTCTATcTTCTTGCTGGCCcTACTGTCC
127	T9	489 TTATGCAACAGGAAcTACCtGGTTGCTCtTTTTCTATcTTCTTGCTGGCCcTACTGTCC
125-128	consensus	TTATGCAACAGGgAAcTACC - GGTTGCTCcTTTTTCTATcTTCTTGCTgGCCcTaCTGTCC
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	550 TGCATCActATTCCgGttTCaGCT
125	T4	550 TGCATCACCATTCCAGTCTCcGCT
126	US10	550 TGCATCACCATTCCAGTCTCTGCT
127	T9	550 TGCATCACCACtCCgGcCTCTGCT
125-128	consensus	TGCATCACCcAtTCC - GtcTctGCT

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FIGURE 6E-1

SEQ ID NO:	ISOLATE	
131	DK11	1 ATGAGCACAAATCCTAAACCTCAAAGAAACCCAAAGAAATACAAACCGCGCCACAGG
132	SW3	1 ATGAGCACAAATCCTAAACCTCAAAGAAACCCAAAGAAATACAAACCGCGCCACAGG
133	DK8	1 ATGAGCACAAATCCTAAACCTCAAAGAAACCCAAAGAAACACAAACCGCGCCACAGG
129	T8	1 ATGAGCACAAATCCTAAACCTCAAAGAAACCCAAAGAAACACAAACCGCGCCACAGG
130	US1	1 ATGAGCACAAATCCTAAACCTCAAAGAAACCCAAAGAAACACAAACCGCGCCACAGG
129-133	consensus	ATGAGCACAAATCCTAAACCTCAAAGAAACCCAAAGAAACACAAACCGCGCCACAGG
SEQ ID NO:	ISOLATE	
131	DK11	62 ACGTTAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
132	SW3	62 ACGTTAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
133	DK8	62 ACGTTAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
129	T8	62 ACGTCAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
130	US1	62 ACGTCAAGTTCCCGGTGGCGGTCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
129-133	consensus	ACGTTAAGTTCCCGGTGGCGGcCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
SEQ ID NO:	ISOLATE	
131	DK11	123 CCCAGGTTGGGTGTGCGCaCGACAAGGAAGACTTCGAGCGATCCCAGCCGCGTGGGAGA
132	SW3	123 CCCAGGTTGGGTGTGCGCGCGACAAAGGAAGACTTCGAGCGATCCCAGCCGCGTGGGAGA
133	DK8	123 CCCAGGTTGGGTGTGCGCGCGACAAAGGAAGcCTTCGAGCGATCCCAGCCGCGTGGGAGg
129	T8	123 CCcTAGGTTGGGTGTGCGCGCGACAAAGGAAGACTTCGAGCGATCCCAGCCGCGTGGGAGA
130	US1	123 CCCAGGTTGGGTGTGCGCGCGACAAAGGAAGACTTCGAGCGATCCCAGCCGCGTGGGAGA
129-133	consensus	CCCcAGGTTGGGTGTGCGGcCGACAAGGAAGaCTTCGAGCGATCCCAGCCGCGTGGGAGa

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FIGURE 6E-2

SEQ ID NO:	ISOLATE
131	DK11
132	SW3
133	DK8
129	T8
130	US1
129-133	consensus
184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGcCCTGGGAAAGCCAGGATATC 184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAAGCCAGGATATC 184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAAGCCAGGATATC 184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAAGCCAGGATATC 184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAAGCCAGGATATC	
CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAAGCCAGGATATC	
SEQ ID NO:	ISOLATE
131	DK11
132	SW3
133	DK8
129	T8
130	US1
129-133	consensus
245 CTTGGCCCCCTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG 245 CTTGGCCCCCTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG 245 CTTGGCCCCCTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG 245 CTTGGCCTCTtTACGGAAACGAGGGCTGCGGtTGGCAGGTTGGCTCCTGTCCCCCGCGG 245 CTTGGCCTCTgTACGGAAACGAGGGCTGCGGcTGGCAGGTTGGCTCCTGTCCCCCGCGG	
CTTGGCCcCTgTAtGGAAACGAGGGCTGCGGcTGGCAGGTTGGCTCCTGTCCCCCGCGG	
SEQ ID NO:	ISOLATE
131	DK11
132	SW3
133	DK8
129	T8
130	US1
129-133	consensus
306 GTCTCATCCTAATTGGGGCCCCCACTGACCCCCCGGCATaATCACGCAATTGGGtAAAGTC 306 GTCTCATCCTAATTGGGGCCCCCACTGACCCCCCGGCATAGATCAGCAATTGGGCAAGTC 306 GTCTCGTCTACTTGGGGCCCCCACTGACCCCCCGGCATAGATCAGCAATTGGGCAAGTC 306 GTCTCGTCTACTTGGGGCCCCCACTGACCCCCCGGCATAGATCAGTAATTGGGCAgAGTC 306 GTCTCGTCTACTTGGGGCCCCCACTGACCCCCCGGCACAGATCAGTAACtTTGGCAagGTC	
GTCTCgTCCTActTTGGGGCCCCCACTGACCCCCCGGCAtAgATCAGCAAtTTGGGCAaaGTC	

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FIGURE 6E-3

SEQ ID NO:	ISOLATE	
131	DK11	367 ATCGACACCATTAACGTGTGGTTTGGCCGACCTCATGGGGTACATCCCTGTCGTcGGCGCCC
132	SW3	367 ATCGACACCATTAACGTGTGGTTTGGCCGACCTCATGGGGTACATCCCTGTCGTtGGCGCCC
133	DK8	367 ATCGACACCATTAACGTGTGGTTTGGCCGACCTCATGGGGTACATCCCTGTCGTtGGCGCCC
129	T8	367 ATCGATACCATTACaTGTGGTTTGGCCGACCTCATGGGGTACATCCCTGTCGTtGGCGCCC
130	US1	367 ATCGATACCATTACgTGTGGTTTGGCCGACCTCATGGGGTACATCCCTGTCGTtGGCGCCC
129-133	consensus	ATCGACACCATTAACgTGTGGTTTGGCCGACCTCATGGGGTACATCCCTGTCGTtGGCGCCC
SEQ ID NO:	ISOLATE	
131	DK11	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGAGTCTTGGAAGACGGGATAAA
132	SW3	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGAGTCTTGGAAGACGGGATAAA
133	DK8	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGAGTCTTGGAAGACGGGATAAA
129	T8	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGAGTCTTGGAAGACGGGATAAA
130	US1	428 CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGAGTCTTGGAAGACGGGATAAA
129-133	consensus	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTTAGgGTCTTGGAAGACGGGATAAA
SEQ ID NO:	ISOLATE	
131	DK11	489 TTACGCAACAGGGAATCTGCCCTGGTTGCTCTTTTCTATCTTCTTACTTGTCTTCTGTcCa
132	SW3	489 TTACGCAACAGGGAATCTGCCCTGGTTGCTCTTTTCTATCTTCTTACTTGTCTTCTGTcCG
133	DK8	489 TTACGCAACAGGGAATTTGCCCTGGTTGCTCTTTTCTATCTTCTTGTCTTGTCTGTcCG
129	T8	489 cTatGCAACAGGGAATTTGCCCTGGTTGCTCTTTTCTATCTTCTTGTCTTGTCTTCTGTcCa
130	US1	489 tTAcGCAACAGGGAATcTGCCCTGGTTGCTCcTTTTCTATCTTCTTaCTTGTCTTCTGTcCG
129-133	consensus	tTAcGCAACAGGGAATcTGCCCTGGTTGCTCtTTTTCTATCTTCTTaCTTGTCTTCTGTcCG

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FIGURE 6E-4

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
131	DK11	550 TGCTgCACAGTGCCAGTGTCTGCCG
132	SW3	550 TGCTtCACAGTGCCAGTGTCTGCCG
133	DK8	550 TGCTgCACAGTGCCAGTGTCTGCCG
129	T8	550 TGCTtCACAGTGCCAGTGTCTGCA
130	US1	550 TGCgcCACgGTGCCgGTGTCTGCA
129-133	consensus	TGct - CACaGTGCCaGTGTCTGCg

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FIGURE 6F-1

SEQ ID NO:	ISOLATE
131	DK11
132	SW3
133	DK8
129	T8C
130	US1
125	T4
126	US10
127	T9
128	T2
134	S83
125-134	consensus
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCGGCCACAGG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCGGCCACAGG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACAAACCGCGGCCACAGG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACAAACCGCGGCCACAGG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACAAACCGCGGCCACAGG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACcAACCGTGGCCACAGG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACtAACCGTGGCCACaAg 1 ATGAGCACAAATCCaAAACCCCAAAGAAAAACCAcAAGAAACACcAACCGTGGCCACAgG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACtAACCGTGGCCACaAg 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACtAACCGcCGCCACAgG ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAaAAGAAACaCaAACCGcCGCCACAgG	
SEQ ID NO:	ISOLATE
131	DK11
132	SW3
133	DK8
129	T8
130	US1
125	T4
126	US10
127	T9
128	T2
134	S83
125-134	consensus
62 ACGTTAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG 62 ACGTTAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG 62 ACGTTAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG 62 ACGTCAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG 62 ACGTCAAGTTCCCGGTGGCGGtCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG 62 ACGTTAAGTTCCCGGTGGCGCCAGATCGTTGGCGGAGTATACTTGTGCCGCGCAGGGG 62 ACGTTAAGTTcCCGGCCGCGCCAGATCGTTGGCGGAGTATACTTGTGCCGCGCAGGGG 62 ACGTTAAGTTcCCGGCCGCGCCAGATCGTTGGCGGAGTATACTTGTGCCGCGCAGGGG 62 ACGTTAAGTTcCCGGCCGCGCCAGATCGTTGGCGGAGTATACTTGTGCCGCGCAGGGG 62 ACGTcAAGTTcCCGGCGGtGGCCAGATCGTTGGCGGAGTATACTTGTGCCGCGCAGGGG ACGTTAAGTTCCCGG - GGcGcCAGATCGTTGGCGGAGT - TACTTGTGCCGCGCAGGGG	

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FIGURE 6F-2

SEQ ID NO.:	ISOLATE
131	DK11
132	SW3
133	DK8
129	T8
130	US1
125	T4
126	US10
127	T9
128	T2
134	S83
125-134	consensus
123	CCCAGGTTGGGTGTGCGCaCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
123	CCCAGGTTGGGTGTGCGCGCGACAAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
123	CCCAGGTTGGGTGTGCGCGCGACAAAGGAAGtCTTCCGAGCGATCCCAGCCGCGTGGGAGg
123	CCctAGGTTGGGTGTGCGCGCGACAAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
123	CCCAGGTTGGGTGTGCGCGCGACAAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
123	CCCAGGTTGGGTGTGCGCGCGACAAAGGAAGACTTCCGAGCGATCCCAGCCACCGTGGGAGG
123	CCCAGGTTGGGTGTGCGCGCGACAAAGGAAGACTTCCGAGCGGTCCCAGCCACCGTGGGAGG
123	CCctAGGTTGGGTGTGCGCaCGACAAGGAAGACTTCCGAGCGGTCCCAGCCACCGTGGGAGG
123	CCCcAGGTTGGGTGTGCGCGCGACAAAGGAAGACTTCCGAGCGGTCCCAGCCctCGTGGaAGg
123	CCcgAGaTTGGGTGTGCGCGCGACgAGGAaAaACTTccGAaCGGTCCCAGCCaCGTGGgAGG
123	CCCcAGgTTGGGTGTGCGCGCGACaAGGAagaCTTccGAgCGaTCCCAGCCgCGTGGgAGg
184	CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAAGcCCTGGGAAAGCCAGGATATC
184	CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAAGTCTCTGGGAAAGCCAGGATATC
184	CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAAGTCTCTGGGAAACCgGGATATC
184	CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAAGTCTCTGGGAAACCAGGATATC
184	CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAAGTCTCTGGGAAAGCCAGGATATC
184	CGCCAGCCCATCCCGAAAGATCGGCGCTCCACTGGCAAGTCTCTGGGAAACCAGGATATC
184	CGCCAGCCCATCCCGAAAGATCGGCGcCCACTGGCAAGTCTCTGGGAAACCAGGATACC
184	CGCCAGCCCATCCCGAAAGATCGGCGCTCCACTGGCAAGTCTCTGGGAAACCAGGATACC
184	CGCCAGCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTCTGGGAAACCAGGATACC
184	CGCCAGCCCATCCCTAAAGATCGGCGCaCCACTGGCAAGTCTCTGGGAAAgCCAGGATACC
125-134	consensus
123	CGCCAGCCCATCCCGAAAGATCGGCGCTCCAC - GGCAAGTCTCTGGGAAaCCaGGATATc

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FIGURE 6F-3

SEQ ID NO:	ISOLATE
131	DK11
132	SW3
133	DK8
129	T8
130	US1
125	T4
126	US10
127	T9
128	T2
134	S83
125-134	consensus

245	CTTGGCCCTGTATGGAACGAGGGCTGGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
245	CTTGGCCCTGTATGGAACGAGGGCTGGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
245	CTTGGCCCTGTATGGAACGAGGGCTGGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
245	CTTGGCCCTCTTACGGAACGAGGGCTGGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
245	CTTGGCCCTGTACGGAACGAGGGCTGGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
245	CcTGGCCCTGTATGGAATGAGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
245	CtTGGCCCTATATGGAATGAGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
245	CCTGGCCCTATATGGAATGAGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
245	CCTGGCCCTGTATGGAATGAGGGCTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
245	CtTGGCCCTGTATGGAATGAGGGCTCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
CtTGGCCCTGTATGG-AA-GAGGGc--CGGcTGGGcAGGtTGGCTCCTGTCCCCCGCGG	

306	GTCTCATCCTAATTGGGGCCCCACTGACCCCCCGCATaATCACGCAATTTGGGtAAAGTC
306	GTCTCATCCTAATTGGGGCCCCACTGACCCCCCGCATAGATCACGCAATTTGGGCAAGTC
306	GTCTCGTCCTACTTGGGGCCCCACTGACCCCCCGCATAGATCACGCAATTTGGGCAAGTC
306	GTCTCGTCCTACTTGGGGCCCCACTGACCCCCCGCATAGATCACGTAATTTGGGCAAGTC
306	GTCTCGTCCTACTTGGGGCCCCACTGACCCCCCGGcAcAGATCACGTAACTTGGGCAAGTC
306	TTCCCGTCCCTCcTGGGGCCCCAaTGACCCCCCGCATAGGTCCGCAACGTGGTAAGGTC
306	TTCCCGTCCCTCTTGGGGCCCCAcTGATCCCCCGCATAGGTCCGCAACGTGGTAAGGTC
306	TTCCCGTCCCTCTTGGGGCCCCAcTGACCCCCCGCATAGGTCCGCAACGTGGTAAGGTC
306	TTCTCGTCCCTCTTGGGGCCCCAaTGACCCCCCGCATAGGTCCGCAATGTGGTAAGTC
306	TTCTCGcCCTTCaTGGGGCCCCAcCGACCCCCCGCATaTCCGCAAcTGGTAAGTC
-TcTcGtCcT-ctTGGGGCCCCAcTgAcCCCCCGCATAgATC-CGcAA-tTGGGtAa-GTC	

131	DK11
132	SW3
133	DK8
129	T8
130	US1
125	T4
126	US10
127	T9
128	T2
134	S83
125-134	consensus

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FIGURE 6F-4

SEQ ID NO:	ISOLATE	
131	DK11	367 ATCGACACCAATTACGTGTGGTTTGGCCGACCTCATGGGGTACATCCCTGTCTCGTcGGCGCCC
132	SW3	367 ATCGACACCAATTACGTGTGGTTTGGCCGACCTCATGGGGTACATCCCTGTCTCGTtGGCGCCC
133	DK8	367 ATCGACACCAATTACGTGTGGTTTGGCCGACCTCATGGGGTACATCCCTGTCTCGTtGGCGCCC
129	T8	367 ATCGATACCAATTACaTGtGGTTTGGCCGACCTCATGGGGTACATCCCTGTCTCGTtGGCGCCC
130	US1	367 ATCGATACCAATTACGTGTGGTTTGGCCGACCTCATGGGGTACATCCCTGTCTCGTtGGCGCCC
125	T4	367 ATCGATACCCTAACGTGCaGcTTGGCCGACCTCATGGGGTACgTCCCCGTCTaGGCGGCC
126	US10	367 ATCGATACCCTAACGTGCGGCTTGGCCGACCTCATGGGaTACATCCCCGTCTgGGCGCtC
127	T9	367 ATCGATACCCTAACGTGCGGCTTGGCCGACCTCATGGGGTACATCCCCGTCTGTAGGGCGCCC
128	T2	367 ATCGATACCCTAACGTGCGGCTTGGCCGACCTCATGGGGTACATCCCCGTCTGTAGGGCGCCC
134	S83	367 ATCGATACCCTAACGTGCGGtTTTGGCCGACCTCATGGGGTACATaCCCCGTCTGTtGGCGCtC
125-134	consensus	ATCGAtACC-T-ACgTG-ggttTTGGCCGACCTCATGGGgTACaTcCC-GTCGTtGGCGccc
428	DK11	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTAGAGTCTCTGGAAGACGGGATAAA
428	SW3	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTAGAGTCTCTGGAAGACGGGATAAA
428	DK8	CGGtGGAGGCGTCGCCAGAGCTCTGGCACACCGGTGTAGGTCTCTGGAAGACGGGATAAA
428	T8	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACaTGGTGTAGGTCTCTGGAAGACGGGATAAA
428	US1	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACaCGGTGTAGGTCTCTGGAAGACGGGATAAA
428	T4	CGtTgGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGaGTCTCTGGAGGACGGGGTTAA
428	US10	CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGTCTCTGGAGGACGGGGTTAA
428	T9	CGCTTGGTGGCGTtGCCAGAGCTCTCGCGCaCGCGTGAGAGTCTCTGGAGGACGGGGTTAA
428	T2	CGCTTGGTGGtGTcGCCAGAGCTCTtGCCCATGGCGTGAGAGTCTCTGGAGGACGGGaGTTAA
428	S83	CcgTTGGcGGcGtTtGCCAGAGCcCTcGccCATGGgGTGAGgGtTCTGGAGGACGGGgaTaaa
125-134	consensus	CggTtGGaGGcGTcGCCAGAGctCTgGCaCA-GGtGT-AG-GTcCTGGA-GACGGGgaTaaa

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FIGURE 6F-5

SEQ ID NO:	ISOLATE	
131	DK11	489 TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTCTATCTTCTTACTTGTCTCTTCTGTCa
132	SW3	489 TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTCTATCTTCTTACTTGTCTCTTCTGTcG
133	DK8	489 TTACGCAACAGGGAATTTGCCCTGGTTGCTCTTTTCTATCTTCTTGTCTCTTCTGTcG
129	T8	489 cTAtGCAACAGGGAATTTGCCCTGGTTGCTCTTTTCTATCTTCTTGTCTCTTCTGTcCa
130	US1	489 TTAcGCAACAGGGAATcTGCCCTGGTTGCTCTTTTCTATCTTCTTaCTTGTCTCTTCTGTcG
125	T4	489 TTATGCAACAGGGAACCTTACCTGGTTGCTCTTTTCTATCTTCTTGTGGCCCTACTGTcC
126	US10	489 TTATGCAACAGGGAACCTTACCCGGTTGCTCTTTTCTATCTTCTTGTGGCCCTACTGTcC
127	T9	489 TTATGCAACAGGGAACcTAcCtGGTTGCTCTTTTCTATCTTCTTGTGGCCCTACTGTcC
128	T2	489 TTATGCAACAGGtAACTTACCCGGTTGCTCcTTTCTATCTTCTTGTaGCCCCTgCTGTcC
134	S83	489 TTATGCAACgGGgAAAtTTgCCGGTTGCTCtTtCTATCTTcTctTgGCCCCtctTGtCt
125-134	consensus	tTAtGCAACaGGgAAAtTgCctGGTTGCTCtTtTcTATcTtTctTgcTtGC-cTtcTGTCc
131	DK11	550 TGCTgCACAGTGCCAGTGTCTGCG
132	SW3	550 TGCTtCACAGTGCCAGTGTCTGCG
133	DK8	550 TGCTgCACAGTGCCAGTGTCTGCG
129	T8	550 TGCTtCACAGTGCCAGTGTCTGCA
130	US1	550 TGCgcCACgGTGCCgGTGTCTGCA
125	T4	550 TGCATCACCAATCCAGTCTCcGCT
126	US10	550 TGCATCACCAATCCAGTCTCTGCT
127	T9	550 TGCATCACCAcTCCGGcCTCTGCT
128	T2	550 TGCATCACTATTCGGTTTCaGCT
134	S83	550 TGCATCtCTgTgCCaGTTTCcGCG
125-134	consensus	TGCatCaCagtGCCaGtGTcTGCT

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FIGURE 6G-1

<u>SEQ ID NO:</u> 138	<u>ISOLATE</u> DK12	1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAGAAAAACCAATCCGTCGCCACAGG
135	HK10	1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAGAAAAACCAATCCGTCGCCACAGG
136	S52	1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAGAAAAACCAATCCGTCGCCACAGG
137	S2	1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAGAAAAACCAATCCGTCGCCACAGG
135-138	consensus	ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAGAAAAACCAATCCGTCGCCACAGG
<u>SEQ ID NO:</u> 138	<u>ISOLATE</u> DK12	62 ACGTCAAGTTCCTCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
135	HK10	62 ACGTTAAGTTCCTCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
136	S52	62 ACGTTAAGTTCCTCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
137	S2	62 ACaTcAAGTTCCTCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
135-138	consensus	ACgT-AAGTTCCTCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
<u>SEQ ID NO:</u> 138	<u>ISOLATE</u> DK12	123 CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTcACAGCCTCGCGGACGg
135	HK10	123 CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTcGAGCCTCGCGGACGA
136	S52	123 CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTcACAGCCTCGCGGACGA
137	S2	123 CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTcACAGCCTCGCGGACGg
135-138	consensus	CCCACGATTGGGTGTGCGCGGACGCGTAAACTTCTGAACGGTcACAGCCTCGCGGACG-
<u>SEQ ID NO:</u> 138	<u>ISOLATE</u> DK12	184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCTCTGGGCTCAGCCtGGGTACC
135	HK10	184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCTCTGGGCTCAGCCCGGTACC
136	S52	184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCTCTGGGCTCAGCCCGGTACC
137	S2	184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGgaTCCTGGGCTCAGCCCGGTACC
135-138	consensus	CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCTCTGGGCTCAGCCCGGTACC

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FIGURE 6G-2

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
138	DK12	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGcAGGgTGGCTCCTGTCCCCACGCGG
135	HK10	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGcAGGgTGGCTCCTGTCCCCACGCGG
136	S52	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGcAGGgTGGCTCCTGTCCCCACGCGG
137	S2	245 CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGcAGGgTGGCTCCTGTCCCCACGCGG
135-138	consensus	CTTGGCCCCCTCTATGGTAACGAGGGCTGCGGGTGGGcAGGgTGGCTCCTGTCCCCACGCGG
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
138	DK12	306 CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCCGCGGgGGTCCCGCAATTTTGGGTAAgGTC
135	HK10	306 CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCCGCGGgGGTCCCGCAATTTTGGGTAAgGTC
136	S52	306 CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCCGCGGgGGTCCCGCAATTTTGGGTAAgGTC
137	S2	306 CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCCGCGGgGGTCCCGCAATTTTGGGTAAgGTC
135-138	consensus	CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCCGCGGgGGTCCCGCAATTTTGGGTAAgGTC
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
138	DK12	367 ATCGATACCCCTcACGTGCGGgATTGCCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
135	HK10	367 ATCGATACCCCTcACGTGCGGgATTGCCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
136	S52	367 ATCGATACCCCTcACGTGCGGgATTGCCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
137	S2	367 ATCGATACCCCTcACGTGCGGgATTGCCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
135-138	consensus	ATCGATACCCCTcACGTGCGGgATTGCCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
138	DK12	428 CtGTAGGGGGCGTCGCAAGAGCCCTCGCGCATGGCGTGGGGCCCTTGAAGACGGGATAAA
135	HK10	428 CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGGGGCCCTTGAAGACGGGATAAA
136	S52	428 CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGGGGCCCTTGAAGACGGGATAAA
137	S2	428 CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGGGGCCCTTGAAGACGGGATAAA
135-138	consensus	CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGGGGCCCTTGAAGACGGGATAAA

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FIGURE 6G-3

SEQ ID NO:	ISOLATE	
138	DK12	489 TTTGCAACAGGGAACCTTGCCCGGTTGCTCCTTTTCTATCTTCCCTTCTTGCTCTGTTCTCT
135	HK10	489 TTTGCAACAGGGAACCTTGCCCGGTTGCTCCTTTTCTATCTTCCCTTCTTGCTCTGTTCTCT
136	S52	489 TTTGCAACAGGGAACCTTGCCCGGTTGCTCCTTTTCTATCTTCCCTTCTTGCTCTGTTCTCC
137	S2	489 TTTGCAACAGGGAACCTTGCCCGGTTGCTCTTTTTCTATCTTCCCTTCTTGCCCTGTTCTCT
135-138	consensus	TTT-GCAACAGGGAACCTTGCCCGGTTGCTCcTTTTCTATCTTCCCTTCTTGCTCTGTTCTCTc
SEQ ID NO:	ISOLATE	
138	DK12	550 TGCcTAATTTCATCCAGCAGCTAGT
135	HK10	550 TGCTTAATTTCATCCAGCAGCTAGT
136	S52	550 TGCTTAgtTTCATCCcGCAGCTAGT
137	S2	550 TGCTTAaTTCATCCaGCAGCTAGT
135-138	consensus	TGCTTAaTTCATCCaGCAGCTAGT

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FIGURE 6H-1

<u>SEQ ID NO.:</u> 145	<u>ISOLATE</u> DK13	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAACGTAACCAACCGCGCCCaATGG
143	Z6	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAACGTAACCAACCGCGCCCATGG
144	Z7	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAACGTAACCAACCGCGCCCATGG
140	Z8	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAACGTAACCAACCGCGCCCATGG
139	Z4	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAACGTAACCAACCGCGCCCATGG
142	Z5	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAACGTAACCAACCGCGCCCATGG
141	Z1	1 ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAACGTAACCAACCGCGCCCATGG
139-145	consensus	ATGAGCAGCAATCCTAAACCTCAAAGAAAAACCAACGTAACCAACCGCGCCCATGG
<u>SEQ ID NO.:</u> 145	<u>ISOLATE</u> DK13	62 ACGTTAAGTTCCCGGGTGGcGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
143	Z6	62 ACGTTAAGTTCCCGGGTGGTGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
144	Z7	62 ACGTTAAGTTCCCGGGTGGTGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
140	Z8	62 AtGTAAaTTCCCaGGCGcGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
139	Z4	62 AcGTAAAGTTCCCGGGTGGTGGCCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
142	Z5	62 ATGTAAATTTCCCGGGTGGTGGTcCAGATCGTTGGCGGAGTTTACTTGTGCCGCGCAGGGG
141	Z1	62 ATGTgAAATTTCCCGGGcGGcCAGATCGTTGGCGGAGTTTACTTGTcTGCCCGCGCAGGGG
139-145	consensus	AcGT - AAgTTCCcGGTGGtGGcCAGATCGTTGGCGGAGTTTACTTGTcTGCCCGCGCAGGGG
<u>SEQ ID NO.:</u> 145	<u>ISOLATE</u> DK13	123 CCctAGaTTGGGTGTCCGCGGcACTAGGAAGACTTCGGAGCGGTcGCAACCTCGTGGGAGg
143	Z6	123 CCCcAGgTTGGGTGTCCGCGGcACTAGGAAGACTTCGGAGCGGTcGCAACCTCGTGGGAGa
144	Z7	123 CCCcAGaTTGGGTGTCCGCaCaACTAGGAAGACTTCGGAGCGGTcGCAACCTCGTGGGAGa
140	Z8	123 CCCcAGGTGGGTGTCCGCGGcACTCGGAAGACTTCGGAGCGGTcGCAACCTCGTGGCAGg
139	Z4	123 CCCcAGGTGGGTGTCCGCGGcACTCGaAAGACTTCGGAGCGGTcGCAACCTCGTGGCAGg
142	Z5	123 CCCcAGGTGGGTGTCCGCGGcACTCGGAAGACTTCGGAGCGGTcGCAACCTCGcGGCAGg
141	Z1	123 CCCcGGTTGGGTGTCCGCGGcAgCTCGGAAGACTTCGGAGCGGTcCAACCTCGTGGCAGg
139-145	consensus	CCCcAGgTTGGGTGTGGCGcGCaCTcGgAAGACTTCGGAGCGGTcGCAACCTCGtGGcAGg

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FIGURE 6H-2

<u>SEQ ID NO.</u>	<u>ISOLATE</u>
145	DK13
143	Z6
144	Z7
140	Z8
139	Z4
142	Z5
141	Z1
139-145	consensus
<p>184 CGCCAGCCTATCCCCAAGGCGCGcCaActcGAGGGtAGGTcCTGGGCTCAGCctGGGTATC</p> <p>184 CGCCAGCCTATCCCCAAGGCAAGTcGATCTGAGGAAAGTCTTGGGCTCAGCCCGGTATC</p> <p>184 CGTCAGCCTATCCCCAAGGCAAGTcGATCTGAGGAAAGTCTTGGGCTCaACCCGGGTACC</p> <p>184 CGTCAGCCTATCCCCAAGGCAAGTcGATCTGAGGAAAGTCTTGGGCTCAGCCCGGTACC</p> <p>184 CGTCaACCTATCCCCAAGGCGCGcCaGcCaGAGGGcAGaTCTTGGGcGcAGCCCGGTACC</p> <p>184 CGTCAGCCTATCCCCcAGGcCaCGtCGTCCGAGGGcAGGTCTTGGGCTCAGCCCGGTACC</p> <p>184 CGTCAGCCTATCCCCcAGGcGCGcCGGTCCGAGGGcAGGTCTTGGGCTCAGCCCGGTACC</p> <p>CGtCAGCCTATCCCCaAGGcCaCGtCggtccGAGGGcAGgTCTTGGGCTCAGCCcGGGTAcC</p>	
<u>SEQ ID NO.</u>	<u>ISOLATE</u>
145	DK13
143	Z6
144	Z7
140	Z8
139	Z4
142	Z5
141	Z1
139-145	consensus
<p>245 CtTGGCCcCTTTACGGcAATGAGGGcTcCGGGTGGCGGGATGGCTCCTGTcACCCCGTGG</p> <p>245 CATGGCCCTCTTTACGGTAATGAGGGTtGCGGGTGGCGGGATGGCTCCTGTcACCCCGTGG</p> <p>245 CATGGCCCTCTTTACGGTAACGAGGGTtGCGGGTGGCGAGGATGGCTCtTGTcACCCCGTGG</p> <p>245 CATGGCCCTCTTTACGGTAATGAAGGTGtGGGTGGCGAGGTtGGCTCCTGTcCCCCCGCGG</p> <p>245 CtTGGCCcCTcTATGGCAATGAGGGTcGCGGGTGGCGAGGTGGCTCCTGTcCtCGCGG</p> <p>245 CtTGGCCcCTTTATGGCAATGAGGGTGTGGGTGGCGAGGTGGCTCCTGTcCCCCCGCGG</p> <p>245 CtTGGCCcCTTTACGGCAATGAGGGCTGTGGGTGGCGAGGTGGCTCCTGTcCCCCCGCGG</p> <p>CtTGGCCCTCtTtTAcGGcAAtGAGGGcTgCGGGTGGGGCaGG-TGGCTCtTGTC-CcCGcGG</p>	
<u>SEQ ID NO.</u>	<u>ISOLATE</u>
145	DK13
143	Z6
144	Z7
140	Z8
139	Z4
142	Z5
141	Z1
139-145	consensus
<p>306 CTCTCGgCCGTCTTGGGGcCCgAAATGATCCCCGGCGgAGGTCCCGCAACTTGGGTAAAGTc</p> <p>306 CTCTCGACCGTCTTGGGGtCCAAATGATCCCCGGCGAAGGTCCCGCAACTTGGGTAAAGTc</p> <p>306 CTCTCGACCGTCTTGGGGCCCAATGATCCCCGGCGAAGGTCCCGCAACTTGGGTAAAGTc</p> <p>306 CTCTCGACCGTCTTGGGGCCCAATGATCCCCGGCGGAGGTcCGCGCAATTTGGGTAAAGTc</p> <p>306 CTCTCGGCCATCTTGGGGCCCAATGATCCCCGGCGGAGaTCGCGCAATCTGGGTAAAGTc</p> <p>306 aTCTCGGCCATCTTGGGGCCCAATGATCCCCGGCGTAGGTCCCGCAATCTGGGTAAAGTc</p> <p>306 tTccAGGCCgTCTTGGGGCCcCAATGATCCCCGGCGTAGGTCCCGtAATCTGGGTAAAGTc</p> <p>cTctcGgCCgTCTTGGGGcCCaAATGATCCCCGGCGgAGGTcCCGCAAttTGGGTAAAGTc</p>	

SEQ ID NO:	ISOLATE
145	DK13
143	Z6
144	Z7
140	Z8
139	Z4
142	Z5
141	Z1
139-145	consensus

SEQ ID NO:	ISOLATE
1145	DK13
1143	Z6
1144	Z7
1140	Z8
1139	Z4
1142	Z5
1141	Z1
139-145	consensus

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FIGURE 6H-4

SEQ ID NO:	ISOLATE	
145	DK13	550 TGCCTgACTgTTCCCGctTCGGCC
143	Z6	550 TGCCTaACTgTTCCCaCCTCGGCC
144	Z7	550 TGCCTgACTgTTCCCGCCTCGGCC
140	Z8	550 TGCCTaACcGTcCCAGCGTctGCT
139	Z4	550 TGCCTcACTgTtCCAGCGTCgGCT
142	Z5	550 TGctTGACAAcACcGgGCATCCGCT
141	Z1	550 TGCcTGACAAcACcCaGCATctGCC
139-145	consensus	TGCcTgACTgttCC-gC-TCgGCC

FIGURE 61-1

SEQ ID NO:	ISOLATE	
153	SA11	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCCGCGCCACAGG
152	SA6	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCCGCGCCACAGG
146	SA4	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCCGCGCCACAGG
147	SA5	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCCGCGCCACAGG
148	SA7	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCCGCGCCACAGG
149	SA1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCCGCGCCACAGG
150	SA3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCCGCGCCACAGG
151	SA13	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCCGCGCCACAGG
146-153	consensus	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCCGCGCCACAGG
SEQ ID NO:	ISOLATE	
153	SA11	62 ACGTCAAGTTCCCGGGCGGTGTCAGATCGTTGGTGGAGTTTACTTGTGCCGCGCAGGGG
152	SA6	62 ACGTCAAGTTCCCGGGCGGTGTCAGATCGTTGGTGGAGTTTACTTGTGCCGCGCAGGGG
146	SA4	62 ACGTCAAGTTCCCGGGCGGTGTCAGATCGTTGGTGGAGTTTACTTGTGCCGCGCAGGGG
147	SA5	62 ACGTCAAGTTCCCGGGCGGTGTCAGATCGTTGGTGGAGTTTACTTGTGCCGCGCAGGGG
148	SA7	62 ACGTCAAGTTCCCGGGCGGTGTCAGATCGTTGGTGGAGTTTACTTGTGCCGCGCAGGGG
149	SA1	62 ACGTCAAGTTCCCGGGCGGTGTCAGATCGTTGGTGGAGTTTACTTGTGCCGCGCAGGGG
150	SA3	62 ACGTCAAGTTCCCGGGCGGTGTCAGATCGTTGGTGGAGTTTACTTGTGCCGCGCAGGGG
151	SA13	62 ACGTCAAGTTCCCGGGCGGTGTCAGATCGTTGGTGGAGTTTACTTGTGCCGCGCAGGGG
146-153	consensus	ACGTCAAGTTCCCGGGCGGTGTCAGATCGTTGGTGGAGTTTACTTGTGCCGCGCAGGGG
SEQ ID NO:	ISOLATE	
153	SA11	123 CCCTaGgt.TGGGTGTGCGCGGACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGgCGG
152	SA6	123 CCCTcGta.TGGGTGTGCGCGGACTCGGAAGACTTCgGAACGGTCGCAACCCCGTGGaCGG
146	SA4	123 CCCTAGgT.TGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG
147	SA5	123 CCCTAGaT.TGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG
148	SA7	123 CCCTAGT.TGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG
149	SA1	123 CCCAGGT.TGGGTGTGCGCGGACTCGGAAGACTTCgGAACGGTCGCAACCCCGTGGGCGG
150	SA3	123 CCCAGGT.TGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGACGG
151	SA13	123 CCCTAGGT.TGGGTGTGCGCGCaACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGACGG
146-153	consensus	CCCTaGgt.TGGGTGTGCGCGGcACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGgCGG

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FIGURE 6I-2

SEQ ID NO:	ISOLATE
153	SA11
152	SA6
146	SA4
147	SA5
148	SA7
149	SA1
150	SA3
151	SA13
146-153	consensus
184	CGTCAGCCTATTCCCAAGGCGGCCAACcCaCGGGcCGGTCTCTGGGTCAACCCGGGTACC
184	CGTCAGCCTATTCCCAAGGCGGCCAAAtCcGCGGtCGTCTCTGGGTCAACCCGGGTACC
184	CGCCAGCCTATTCCCAAGGCGGCCAACCCACGGGCCGTCTCTGGGTCAACCCGGGTACC
184	CGCCAGCCTATTCCCAAGGCGGCCAACCCACGGGCCGTCTCTGGGTCAACCCGGGTACC
184	CGCCAGCCTATTCCCAAGGCGGCCAACCCACGGGCCGTCTCTGGGTCAACCCGGGTACC
184	CGCCAGCCTATTCCCAAGGCGGCCAACCCACGGGCCGTCTCTGGGTCAACCCGGGTACC
184	CGCCAGCCTATTCCCAAGGCGGCCAACCCACGGGCCGTCTCTGGGTCAACCCGGGTACC
184	CGCCAGCCTATTCCCAAGGCGGCCAACCCACGGGCCGTCTCTGGGTCAACCCGGGTACC
184	CGtCAGCCTATcCCCAAGGcGCGCCAGCCcCACGGGCCGTCTCTGGGTCAACCCGGGTACC
146-153	CGcCAGCCTATTcCCCAAGGcGCGCCAacCCaCGGGcCGGTCTCTGGGTCAACCCGGGTACC
SEQ ID NO:	ISOLATE
153	SA11
152	SA6
146	SA4
147	SA5
148	SA7
149	SA1
150	SA3
151	SA13
146-153	consensus
245	CTTGGCCCTTTACGCCCAATAGGGCCCTCGGGTGGGcAGGTGGcTGCTCTCCCCtCGAGG
245	CTTGGCCCTTTACGCCCAATAGGGCCCTCGGGTGGGcAGGTGGtTGCTCTCCCCCGAGG
245	CTTGGCCCTTTACGCCCAATAGGGCCCTCGGGTGGGcAGGTGGtTGCTCTCCCCCGAGG
245	CTTGGCCCTTTACGCCCAATAGGGCCCTCGGGTGGGcAGGTGGtTGCTCTCCCCCGAGG
245	CTTGGCCCTTTACGCCCAATAGGGCCCTCGGGTGGGcAGGTGGtTGCTCTCCCCCGAGG
245	CTTGGCCCTTTACGCCCAATAGGGCCCTCGGGTGGGcAGGTGGtTGCTCTCCCCCGAGG
245	CTTGGCCCTTTACGCCCAATAGGGCCCTCGGGTGGGcAGGTGGtTGCTCTCCCCCGAGG
245	CTTGGCCCTTTACGCCCAATAGGGCCCTCGaGTGGGcAGGTGGtTGCTCTCCCCCGAGG
245	CTTGGCCCTTTAtGCCAATAGGGCCCTCGgGTGGGcAGGTGGtTGCTCTCCCCCGAGG
146-153	CTTGGCCCTTTAcGCCAATAGGGCCCTCGgGTGGGcAGGTGGtTGCTCTCCCCCGAGG
SEQ ID NO:	ISOLATE
153	SA11
152	SA6
146	SA4
147	SA5
148	SA7
149	SA1
150	SA3
151	SA13
146-153	consensus
306	CTCTCGGCCCTAAcTGGGGCCCCCAATGACCCCCCGCGGAAGATCGCGCAATTtTGGGcAAGGTC
306	CTCTCGGCCCTAAcTGGGGCCCCCAATGACCCCCCGCGGAATcCGCGCAATTtTGGGTAAAGTC
306	CTCTCGGCCCTAAcTGGGGCCCCCAATGACCCCCCGCGGAAGTcCGCGCAATTtTGGGTAAAGTC
306	CTCTCGGCCCTAAcTGGGGCCCCCAATGACCCCCCGCGGAATcCGCGCAATTtTGGGTAAAGTC
306	CTCTCGGCCCTAAcTGGGGCCCCCAATGACCCCCCGCGGAAGTcCGCGCAATTtTGGGTAAAGTC
306	CTCTCGGCCCTAAcTGGGGCCCCCAATGACCCCCCGCGGAAGTcCGCGCAATTtTGGGTAAAGTC
306	CTCTCGGCCCTAAcTGGGGCCCCCAATGACCCCCCGCGGAAGTcCGCGCAATTtTGGGTAAAGTC
306	CTCTCGGCCCTAgTGGGGCCCCCAAcGACCCCCCGCGGAATcCGCGCAATTtTGGGTAAAGTC
306	CTCTCGGCCCTAaTtTGGGGCCCCCAATGACCCCCCGCGGAATcCGCGCAAcTTtTGGGTAAAGTC
146-153	CTCTCGGCCCTAAtTGGGGCCCCCAAtGACCCCCCGCGGAaAaTcCGCGCAAtTTtTGGGTAAAGTC

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FIGURE 61-3

SEQ ID NO:	ISOLATE	
153	SA11	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
152	SA6	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
146	SA4	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
147	SA5	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
148	SA7	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
149	SA1	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
150	SA3	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
151	SA13	367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
146-153	consensus	ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
SEQ ID NO:	ISOLATE	
153	SA11	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACACGGTGTGAGAGcTCTTGAGGACGGGGTAAA
152	SA6	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACACGGTGTGAGAGTCTTGAGGACGGGGTAAA
146	SA4	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACATGTTGTGAGGGTCTTGAGGACGGGGTAAA
147	SA5	428 CCGTTGGGGCGTCGCAAGGGCCCTCGCACATGTTGTGAGGGTCTTGAGGACGGGGTAAA
148	SA7	428 CCGTTGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGTCTTGAGGACGGGGTAAA
149	SA1	428 CCGTTGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGTCTTGAGGACGGGGTAAA
150	SA3	428 CCGTTGGGGCGTCGCAAGGGCTCTCGCACATGGTGTGAGGGTCTTGAGGACGGGGTAAA
151	SA13	428 CCGTTGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGTCTTGAGGACGGGGTAAA
146-153	consensus	CCGTTGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGgGctCTTGAGGACGGGGTAAA
SEQ ID NO:	ISOLATE	
153	SA11	489 tTATGCAACAGGGAATcttCCCGGTGCTCTTTCTCtATCTTTaTCCTTGCACTTCTCTCG
152	SA6	489 CTATGCAACAGGGAATTTGCCCGGTGCTCTTTCTCTATCTTTgTCCTTGCACCTTCTCTCG
146	SA4	489 CTATGCAACgGGGAATTTGCCCGGTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG
147	SA5	489 CTATGCAACAGGGAATTTGCCCGGTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG
148	SA7	489 tTACGCAACAGGGAATcTGCCCGGTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG
149	SA1	489 CTACGCAACAGGGAATTTGCCCGGTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCC
150	SA3	489 CTACGCAACAGGGAATTTACCCCGGTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCA
151	SA13	489 CTAtGCAACAGGGAATTTACCCCGGTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCA
146-153	consensus	cTAtGCAACaGGGAATtTgCCCGGTGCTCTTTCTCTtATCTTTaTCCTTGCACTTCTCTcTcg

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FIGURE 6I-4

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
153	SA11	550 TGctTgACCGTCCCgGCCaCTGCA
152	SA6	550 TGCCTaACCGTCCCtGCCCTCTGCA
146	SA4	550 TGCCTGACCGTCCCgGCCCTCTGCA
147	SA5	550 TGctTGACCGTCCCAGCCTCTGCA
148	SA7	550 TGCCTGACCGTCCCAGCCTCcGCA
149	SA1	550 TgtCTGAtCaTCCGGCCTCTGCA
150	SA3	550 TGCCTGACCGTCCCAGCCTCTGCA
151	SA13	550 TGCCTGACTGTCCCGaCCTCTGCC
146-153	consensus	TGccTgAccgTCCCggCCtCtGCa

FIGURE 6J-1

<u>SEQ ID NO:</u>	<u>Genotype</u>
103-154	cons.
1	ATGAGCACgaaTCCTAAACCTCAAAGAAaAaACCaaAcGtAAcACcAaCCgcCGCCcCacagG
103-124	1
125-134	2
135-138	3
139-145	4
146-153	5
154	6
1	ATGAGCACgAaTCCTAAaACCTCAAAGAAaAaACCAAAACGTAAACACCAaCCgcCGCCcCACAGG
1	ATGAGCACAAaTCCTAAACCTCAAAGAAaAaACCAAAACCAaAGAAAcACaAACCCcCGCCcCACAGG
1	ATGAGCACACTTCCTAAACCTCAAAGAAaAaACCAAAACCAaAGAAAcACCAATCCGTCCGCCACAGG
1	ATGAGCACgAATCCTAAACCTCAAAGAAaAaACCAAAACCAaAGAAAcACCAATCCGTCCGCCcATGG
1	ATGAGCACGAATCCTAAACCTCAAAGAAaAaACCAAAACCAaAGAAAcACCAATCCGTCCGCCcACAGG
1	ATGAGCACACTTCCAAaACCCCAaAGAAaAaACCAAAACCAaAGAAAcACCAACCGTCGCCcCAACGG
62	AcgTcAAgTTcCCgGGcGGtGGtCAGATCGTtGGtGGAGTtTActTgtTGCCGCGCAGGGG
62	ACGTcAAgTTCCCGGGcGGtGGtCAGATCGTtGGTGGAGTtTAccTgTTGCCGCGCAGGGG
62	ACGTtAAgTTCCCGGGcGGcGGcCAGATCGTtGGCGGAGTaTACTTgcTGCCGCGCAGGGG
62	AcgTcAAgTTCCCGGGTGGCGGACAGATCGTtGGTGGAGTATACGTgTTGCCGCGCAGGGG
62	AcGTaAaGTTCCCGGGtGGtGGcCAGATCGTtGGCGGAGTtTACTTgtTGCCGCGCAGGGG
62	ACGTcAAgTTCCCGGGCGGTGGTcAGATCGTtGGTGGAGTtTACTTgTTGCCGCGCAGGGG
62	ACGTcAAgTTCCCGGGTGGCGGTcAGATCGTtGGCGGAGTtTACTTgTTGCCGCGCAGGGG
123	CCCCaGgtTGGGTGTGGCGGcGgaCtaGgAAgaCTTCcGAgCGgTCgCAaCCtcGtGGaaGg
123	CCCCaGgtTTGGGTGTGGCGGCGgaCtAGGAAGACTTCcGAGCGgTCgCAACCTCGtGGaaGg
123	CCCCaGgtTTGGGTGTGGCGGCGGCGAGCaAGGAAGaCTTCcGAgCGaTCCAGCCcCGTGGgAGg
123	CCCCAGATTTGGGTGTGGCGGCGGACCGGTAAaACTTCtGAACGGTcACAGCCTCGCGGACGa
123	CCCCaGgtTTGGGTGTGGCGGCGgCgaCTcGgAAGACTTCGGAGCGGTcGCAACCTCGtGGcAGg
123	CCctaGgtTTGGGTGTGGCGGCGgACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGgCGG
123	CCCCCGGTGGGTGTGGCGGCGGACGAGAAAGACTTCcGAGCGATCCcAGCCcCAGAGGGCAGG
103-124	1
125-134	2
135-138	3
139-145	4
146-153	5
154	6
103-124	1
125-134	2
135-138	3
139-145	4
146-153	5
154	6
103-124	1
125-134	2
135-138	3
139-145	4
146-153	5
154	6
103-124	1
125-134	2
135-138	3
139-145	4
146-153	5
154	6

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FIGURE 6J-2

SEQ ID NO:	Genotype		
103-154	cons.		
184		CGaCagCctATcCCcaAgGctCGcCgccccgagGGcaggtcCTGGGctcagCCcGGgtAcC	
184	1	CGaCAaCCtATCCCCAAGGctCGcCgCCCCGAGGgcAGGgCCTGGGctCAGCCCcGGgtAcC	
125-134	2	CGCCAGCCCCATCCgAAAGATCGGGCctCCActGGCAAGtCCTGGGGAaaCCaGGATAtC	
135-138	3	CGACAGCCTATCCCCAAGGCGCTCGAGCGAAGCCGgTCTGGGCTCAGCCCcGGGTACC	
139-145	4	CGtCAGCCTATCCCCaAGGCaCGtCggtccGAGGgcAGgTCTTGGGctCAGCCCcGGGTAcC	
146-153	5	CGcCAGCCTATtCCCCAAGGcGCGCCAAcCCaCGGGcCGGTCTTGGGgtCAACCCGGGTACC	
154	6	CGCCAACCTATACCAAGGCGCGCCAGCCCCAGGCaGGCaCTGGGCTCAGCCCCGGATACC	
SEQ ID NO:	Genotype		
103-154	cons.		
245		CtTGGCCccTcTAtGgcaATGAgGGcttcGggTGGGCaGgaTGGcTccTgTCCcCCcCgCGG	
245	1	CtTGGCCCCCTCTAtGgCaATGAGGGcttgGGgTGGGCaGGATGGCTCCTGTCaCCCCgtGG	
125-134	2	CtTGGCCcCTgTAtGGgAAATGAGGGcctCGGcTGGGCaGGtTGGCTCCTGTCCCCCGcGG	
135-138	3	CtTGGCCCCCTCTATGGTAACGAGGGCTGCGGTGGGCaGGgTGGCTCCTGTCCCCACGCGG	
139-145	4	CtTGGCCctCTtTAcGGcAAATGAgGGcTgCGGGTGGGCaGGgTGGCTCcTGTCCcCCcCGcGG	
146-153	5	CtTGGCCCCcTTTAcGCCAAATGAGGGcCTCGgGTGGGCaGGGTGGtTGCTCTCCCCcCGAGG	
154	6	CtTGGCCCTCTTTATGGAAACGAGGGCTGTGGGTGGGCaGGTTGGCTCCTGTCCCCCGCGG	
SEQ ID NO:	Genotype		
103-153	cons.		
306		cTctcggCCtagtTGGGGcCccActGAcCCCCGGCgtaggTCgCGcAAttTGGGtAagGTC	
306	1	cTctCGGCCTAgT TGGGGCCCCcAcaGACCCCCCGGCGtAGGTCCGCGtAAttTGGGtAAGGTC	
125-134	2	tTctCgtCCtctctTGGGGCCCCActGAcCCCCGGCaTAgATCgCGcAActTGGGtAagGTC	
135-138	3	CTCCCGTCCATCTTGGGGCCCCAAAGAcCCCCCGGCGgaGGTCCCGCAATTTGGGTAAGTC	
139-145	4	cTctcGgCCgTCTTGGGGcCcaAATGATCCCCCGGCGgAGgTCCCGcAAttTGGGTAAGGTC	
146-153	5	CTCTCGGCCTAatTGGGGCCCCCAATGACCCCCGGCGGaAaATCGCGCAATTTGGGtAAGGTC	
154	6	CTCCCGGCCACAT TGGGGCCCCCAATGACCCCCCGGCGTCCGATCCCGGAATTTGGGTAAGGTC	

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FIGURE 6J-3

SEQ ID NO:	Genotype	
103-154	cons.	
103-124	1	ATCGATACccTcACgTGcgGctTcGCCGAcCTCATGGGgTACaTcCCgcTCGTcGGcGccc
125-134	2	ATCGATACcCTcACaTGGGGTTcGCCGACCTCATGGGGTACATtCCGCTCGTCGGcGccc
135-138	3	ATCGATACcCTaACgTGcgGttTTGCCGACCTCATGGGgTACaTcCCcGTcGTtGGCGccc
139-145	4	ATCGATACcCTtACGTGGGgATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
146-153	5	ATCGATACcCTgACgTGcgGcTTcGCCGACCTCATGGGGTACATcCCGcTCGTaGGCGCCC
154	6	ATCGATACcCTaACgTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTAGCGGGCC
		ATCGATACcCTAACGTGTGGTTTCGCCGATCTCATGGGGTACATTCGCCGTCTGTGGCGCGC
SEQ ID NO:	Genotype	
103-154	cons.	
103-124	1	CcgTaGGGGGcGtcGCCaggGCCcTgGCgCATGGcGTcaGgggttcTgAGAGACGGggTgAA
125-134	2	CccTaGGGGGcGcTGCCAGGGCCcTGGCGcATGGcGTCCGGGTtcTGGAGGACGGCGTGAA
135-138	3	CggTtGGaGGcGTcGCCAGAGcCTtGgCaCATGGtGTgAGgGTcCTGGAGGACGGgaTaaa
139-145	4	CcGTAGGaGGCGTCGCAAGAGCCCTCGCGCATGGCGTgAGGGCCCTTGAAGACGGGATAAA
146-153	5	CcGTgGgtGGCGTCGCCAGGGCCcTgGCgCATGGcGTcAGGgctgTGGAGGACGGgaTcaa
154	6	CCGTtGGGGCGTCGCAAGGGcCTcTcGCACACGGTGTGAGgGtctCTTGAGGACGGGGTAAA
		CtTTGGGGCGCGTCGGCGCTCGCGCTCGCACATGGCGTGAGGGCAATCGAGGACGGGATCAA
SEQ ID NO:	Genotype	
103-154	cons.	
103-124	1	cTatGCAACaGGgAAttTgCCCgGTTGCTCtTtTcTcTATcTtTccTccTgcTgTcc
125-134	2	cTAtGCAACAGGGAAtcTgCCCgGTTGCTCtTtTcTCTATCTTCTcTtTgGCTtTgTgTcc
135-138	3	tTAtGCAACaGGgAAttTgCctGGTTGCTCtTtTtTCTATcTtTctTgTtGCCcTtcTGTCc
139-145	4	TTTcGCAACAGGGAACTTgCCCCGGTTGCTCtTtTtTCTATCTTCTTCTTGTCTCTcT
146-153	5	cTAtGCAACAGGGAAcCTTCCcGGTTGCTCtTtTcTCTATCTTcTctTgGCACTtcTcTCG
154	6	cTAtGCAACaGGgAAttTgCCCCGGTTGCTCtTtTCTcTATcTtTaTCCTTGCACTTCTcTCg
		TTATGCAACAGGGAACTCTCCCCGGTTGCTCtTtTCTCTATCTTCTTtTGGCACTACTCTCG

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FIGURE 6J-4

SEQ ID NO:	Genotype	
103-154	cons.	
103-124	1	550 TGcctgaccgtcCCagcttCtgct
125-134	2	550 TGttTgACcatcCCaGctTCCGct
135-138	3	550 TGCatCaCagtGCCaGtGTctGct
139-145	4	550 TGctTAaTTCATCCaGCAGCTAGT
146-153	5	550 TGCcTgACTgttCCagCgTCgGCC
154	6	550 TGccTgAccgTCCCggCCctCtGCa
		550 TGCCTCACAAACGCCAGCTTCGGCT

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FIGURE 6K-1

SEQ ID NO:	Genotype	10	20	30	40	50	60	70	80	90	100	110
103-108	1/1a	ATGAGCAG	gaatcc	taaacct	caaaagaa	aaaccc	aaagaa	gcgcgc	ccacag	gcagag	gcagag	gcagag
109-124	1/1b	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
125-128	1/1/2a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
129-133	1/1/2b	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
134	2c	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
135-138	(V)/3a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
139	4a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
141	4b	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
143	4c	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
145	4d	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
146-153	5a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
154	6a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c

SEQ ID NO:	Genotype	120	130	140	150	160	170	180	190	200	210	220	230
103-108	1/1a	gcagggcc	cccgag	tggtgt	ggtgtg	ggtgtg	ggtgtg	ggtgtg	ggtgtg	ggtgtg	ggtgtg	ggtgtg	ggtgtg
109-124	1/1b	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c	g-c
125-128	1/1/2a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c	g-c
129-133	1/1/2b	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c	g-c
134	2c	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c	g-c
135-138	3a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c	g-c
139	4a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c	g-c
141	4b	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c	g-c
143	4c	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c	g-c
145	4d	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c	g-c
146-153	5a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c	g-c
154	6a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c	g-c

SEQ ID NO:	Genotype	240	250	260	270	280	290	300	310	320	330	340
103-108	1/1a	tcagccgg	taaccct	tggtgt	ggtgtg	ggtgtg	ggtgtg	ggtgtg	ggtgtg	ggtgtg	ggtgtg	ggtgtg
109-124	1/1b	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
125-128	1/1/2a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
129-133	1/1/2b	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
134	2c	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
135-138	3a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
139	4a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
141	4b	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
143	4c	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
145	4d	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
146-153	5a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c
154	6a	gaa-t	t	a-a	aa-c	t-c	c-a	gt	acag	cg-c	g-c	g-c

[illegible]

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FIGURE 7A-1

SEQ ID NO:	ISOLATE	
156	US11	1 MSTNPKPQRKTKRNTNRRPQDVKFFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
157	S14	1 MSTNPKPQRKTKRNTNRRPQDVKFFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
158	SW1	1 MSTNPKPQRKTKRNTNRRPQDVKFFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
159	S18	1 MSTNPKPQRKTKRNTNRRPQDVKFFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
160	DR4	1 MSTNPKPQRKTKRNTNRRPQDVKFFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
155	DK7	1 MSTNPKPQRKTKRNTNRRPQDVKFFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
155-160	consensus	MSTNPKPQRKTKRNTNRRPQDVKFFPGGGQIVGGVYLLPRRGPRLGVRA TRKTSERSQPRGR
SEQ ID NO:	ISOLATE	
156	US11	62 ROIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
157	S14	62 ROIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
158	SW1	62 ROIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
159	S18	62 ROIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
160	DR4	62 ROIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
155	DK7	62 ROIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
155-160	consensus	ROIPKARRPEGRTWAQPGYPWPPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
SEQ ID NO:	ISOLATE	
156	US11	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLALLS
157	S14	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLALLS
158	SW1	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLALLS
159	S18	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLALLS
160	DR4	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLALLS
155	DK7	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLALLS
155-160	consensus	IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDDGVNYATGNLPGCSFSIFLLALLS

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FIGURE 7A-2

SEQ ID NO:	ISOLATE	
156	US11	184 CLTVPASA
157	S14	184 CLTVPASA
158	SW1	184 CLTVPASA
159	S18	184 CLTVPASA
160	DR4	184 CLTVPASA
155	DK7	184 CLTVPASA
155-160	consensus	CLTVPASA

FIGURE 7B-1

[illegible]

FIGURE 7B-2

SEQ ID NO.:	ISOLATE
1175	P8
1170	IND8
1162	S45
1171	S9
1163	D1
1165	P10
1169	IND3
1164	US6
1166	DK1
1167	T10
1168	SW2
1161	SA10
1174	HK4
1172	HK3
1176	T3
1173	HK5

161-176 consensus IDTLTCGFADLMGYIPLVGaPLGGaARALAHGVRVLEDGVNYATGNIPGCsFSIFLLALLS

SEQ ID NO:	ISOLATE	CLTiPASA
1175	P8	184 CLTiPASA
1170	IND8	184 CLTvPASA
1162	S45	184 CLTiPASA
1171	S9	184 CLTiPASA
1163	D1	184 CLTiPASA
1165	P10	184 CLTiPASA
1169	IND3	184 CLTiPASA
1164	US6	184 CLTiPASA
1166	DK1	184 CLTiPASA
1167	T10	184 CLTiPASA
1168	SW2	184 CLTiPASA
1161	SA10	184 CLTiPASA
1174	HK4	184 CLTiPASA
1172	HK3	184 CLTtPASA
1176	T3	184 CLTiPASA
1173	HK5	184 CLTtPvSA
161-176	consensus	CLTiPASA

FIGURE 7C-1

SEQ ID NO:	ISOLATE	
173	HK5	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
176	T3	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
172	HK3	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
174	HK4	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
161	SA10	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
168	SW2	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
167	T10	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
166	DK1	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
164	US6	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
169	IND3	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
165	P10	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
163	D1	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
156	US11	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
157	S14	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
158	SW1	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
159	S18	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
160	DR4	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
155	DK7	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
170	IND8	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
162	S45	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
171	S9	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
175	P8	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
155-176	consensus	MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR

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FIGURE 7C-2

SEQ ID NO:	ISOLATE	
173	HK5	62 RQIPKARRPEGRtWAQPGYPWPLYGnEGMGWAGWLLSPhGSRPSWGPTDPRRRSRNLGKV
176	T3	62 RQIPKARRPEGRaWAQPGYPWPLYGdEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
172	HK3	62 RQIPKARQPEGRtWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
174	HK4	62 RQIPKARQPEGRtWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
161	SA10	62 RQIPKARQPEGRtWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
168	SW2	62 RQIPKARQPEGRaWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
167	T10	62 RQIPKARQPEGRaWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
166	DK1	62 RQIPKARRPEGRaWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
164	US6	62 RQIPKARRPEGRaWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
169	IND3	62 RQIPKARRPEGRaWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
165	P10	62 RQIPKARRPEGRaWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
163	D1	62 RQIPKARRPEGRaWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
156	US11	62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
157	S14	62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
158	SW1	62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
159	S18	62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
160	DR4	62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
155	DK7	62 RQIPKARRPEGRtWAQPGYPWPLYGnEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
170	IND8	62 RQIPKARRPEGRaWAQPGHPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
162	S45	62 RQIPKARRPEGRaWAQPGHPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
171	S9	62 RQIPKARhPEGRaWAQPGYPWPLYGnEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
175	P8	62 RQIPKARrPEGRaWAQPGhPWPLYaNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
155-176	consensus	RQIPKARrPEGRaWAQPGYPWPLYGnEG-GWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV

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FIGURE 7C-3

SEQ ID NO:	ISOLATE	
173	HK5	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
176	T3	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
172	HK3	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
174	HK4	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
161	SA10	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
168	SW2	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
167	T10	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
166	DK1	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
164	US6	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
169	IND3	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
165	P10	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
163	D1	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
156	US11	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
157	S14	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
158	SW1	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
159	S18	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
160	DR4	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
155	DK7	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
170	IND8	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
162	S45	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
171	S9	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
175	P8	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS
155-176	consensus	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVDNYATGNIPGCSFSIFLLALLS

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FIGURE 7C-4

SEQ ID NO:	ISOLATE	
173	HK5	184 CLTtPvSA
176	T3	184 CLTiPASA
172	HK3	184 CLTtPASA
174	HK4	184 CLTiPASA
161	SA10	184 CLTtPASA
168	SW2	184 CLTiPASA
167	T10	184 CLTtPASA
166	DK1	184 CLTiPASA
164	US6	184 CLTtPASA
169	IND3	184 CLTiPASA
165	P10	184 CLTtPASA
163	D1	184 CLTiPASA
156	US11	184 CLTtPASA
157	S14	184 CLTiPASA
158	SW1	184 CLTtPASA
159	S18	184 CLTiPASA
160	DR4	184 CLTtPASA
155	DK7	184 CLTiPASA
170	IND8	184 CLTtPASA
162	S45	184 CLTiPASA
171	S9	184 CLTtPASA
175	P8	184 CLTiPASA
155-176	consensus	CLTiPaSA

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FIGURE 7D-1

SEQ ID NO:	ISOLATE	
179	T9	1 MSTNPKPQRKtiRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRtTRKTSERSQPRGR
178	US10	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
180	T2	1 MSTiPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
177	T4	1 MSTnPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
177-180	consensus	MSTnPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRaTRKTSERSQPRGR
SEQ ID NO:	ISOLATE	
179	T9	62 RQIPKDRRsTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGP sDPRHRSRNVGKV
178	US10	62 RQIPKDRRpTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGp tDPRHRSRNVGKV
180	T2	62 RQIPKDRRStTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV
177	T4	62 RQIPKDRRsTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV
177-180	consensus	RQIPKDRRsTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPnDPRHRSRNVGKV
SEQ ID NO:	ISOLATE	
179	T9	123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEdGVNYATGNLPGCSFSiFLLALLS
178	US10	123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEdGVNYATGNLPGCSFSiFLLALLS
180	T2	123 IDTLTCGFADLMGYiPVVGAPLGGVARALAHGVRVLEdGVNYATGNLPGCSFSiFLLALLS
177	T4	123 IDTLTCsIADLMGYvPVVGpLGGVARALAHGVRVLEdGVNYATGNLPGCSFSiFLLALLS
177-180	consensus	IDTLTCgfADLMGYiPVVGaPLGGVARALAHGVRVLEdGVNYATGNLPGCSFSiFLLALLS
SEQ ID NO:	ISOLATE	
179	T9	184 CITtPaSA
178	US10	184 CITiPVSA
180	T2	184 CITiPVSA
177	T4	184 CITiPVSA
177-180	consensus	CITiPVSA

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FIGURE 7E-1

SEQ ID NO:	ISOLATE	
183	DK11	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRtTRKTSERSQPRGR
184	SW3	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRGR
181	T8	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRGR
182	US1	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATRKTSERSQPRGR
185	DK8	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRATRKsERSQPRGR
181-185	consensus	MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRGPRLGVRaTRKtSERSQPRGR
SEQ ID NO:	ISOLATE	
183	DK11	62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHkSRNLGKV
184	SW3	62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHRSRNLGKV
181	T8	62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGrV
182	US1	62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
185	DK8	62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
181-185	consensus	RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGsrPtWGPTDPRHrSRNLGKV
SEQ ID NO:	ISOLATE	
183	DK11	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
184	SW3	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
181	T8	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
182	US1	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
185	DK8	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
181-185	consensus	IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
SEQ ID NO:	ISOLATE	
183	DK11	184 CcTVPVSA
184	SW3	184 CFTVPVSA
181	T8	184 CFTVPVSA
182	US1	184 CaTVPVSA
185	DK8	184 CcTVPVSA
181-185	consensus	C-TVPVSA

FIGURE 7F-1

SEQ ID NO:	ISOLATE	
183	DK11	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVrTrKtSERSQPRGR
184	SW3	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVrTrKtSERSQPRGR
181	T8	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVrTrKtSERSQPRGR
182	US1	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVrTrKtSERSQPRGR
185	DK8	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVrTrKtSERSQPRGR
186	S83	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVrTrKtSERSQPRGR
178	US10	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVrTrKtSERSQPRGR
180	T2	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVrTrKtSERSQPRGR
179	T9	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVrTrKtSERSQPRGR
177	T4	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVrTrKtSERSQPRGR
177-186	consensus	MSTnPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVrTrKtSERSQPRGR
183	DK11	62 RQIPKDRRSTGKpWGKPGYPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHkSRNLGKV
184	SW3	62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHrSRNLGKV
181	T8	62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGrV
182	US1	62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGKV
185	DK8	62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGKV
186	S83	62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHkSRNLGKV
178	US10	62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGKV
180	T2	62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGKV
179	T9	62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGKV
177	T4	62 RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHrSRNLGKV
177-186	consensus	RQIPKDRRSTGKsWGKPGYPWPLYGNEG-GWAGWLLSPRGsrPswGptDPRHrSRNLGKV

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FIGURE 7F-2

SEQ ID NO:	ISOLATE	
183	DK11	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNLPGCSFSIFLLALLS
184	SW3	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNLPGCSFSIFLLALLS
181	T8	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNLPGCSFSIFLLALLS
182	US1	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNLPGCSFSIFLLALLS
185	DK8	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNLPGCSFSIFLLALLS
186	S83	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNLPGCSFSIFLLALLS
178	US10	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNLPGCSFSIFLLALLS
180	T2	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNLPGCSFSIFLLALLS
179	T9	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDDGINYATGNLPGCSFSIFLLALLS
177	T4	123 IDTLTCSLADLMGYVPVVGgPLGGVARALAHGVRVLEDDGINYATGNLPGCSFSIFLLALLS
177-186	consensus	IDT - TCgfADLMGYiPVVGaPvGGVARALAHGVRVLEDDGINYATGNLPGCSFSIFLLALLS
SEQ ID NO:	ISOLATE	
183	DK11	184 CcTVPVSA
184	SW3	184 CFTVPVSA
181	T8	184 CFTVPVSA
182	US1	184 CaTVPVSA
185	DK8	184 CcTVPVSA
186	S83	184 CIsVPVSA
178	US10	184 CITiPVSA
180	T2	184 CITiPVSA
179	T9	184 CITtPaSA
177	T4	184 CITiPVSA
177-186	consensus	CitvPvSA

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FIGURE 7G-1

SEQ ID NO:	ISOLATE	
189	S2	1 MSTLKPQKTKRNTIRRPQDiKFPGGQIVGGVYVLPRRGPRGLGVRATRKTSERSQPRGR
187	HK10	1 MSTLKPQKTKRNTIRRPQDVKFPGGQIVGGVYVLPRRGPRGLGVRATRKTSERSQPRGR
190	DK12	1 MSTLKPQKTKRNTIRRPQDVKFPGGQIVGGVYVLPRRGPRGLGVRATRKTSERSQPRGR
188	S52	1 MSTLKPQKTKRNTIRRPQDVKFPGGQIVGGVYVLPRRGPRGLGVRATRKTSERSQPRGR
187-190	consensus	MSTLKPQKTKRNTIRRPQDVKFPGGQIVGGVYVLPRRGPRGLGVRATRKTSERSQPRGR
SEQ ID NO:	ISOLATE	
189	S2	62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
187	HK10	62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
190	DK12	62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
188	S52	62 RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
187-190	consensus	RQIPKARRSEGRSWAQPYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
SEQ ID NO:	ISOLATE	
189	S2	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
187	HK10	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
190	DK12	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
188	S52	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
187-190	consensus	IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
SEQ ID NO:	ISOLATE	
189	S2	184 CLIHPAAS
187	HK10	184 CLIHPAAS
190	DK12	184 CLIHPAAS
188	S52	184 CLVHPAAS
187-190	consensus	CLIHPAAS

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FIGURE 7H-1

SEQ ID NO:	ISOLATE
194	Z5
193	Z1
192	Z8
195	Z6
196	Z7
191	Z4
197	DK13
191-197	consensus

1	MSTNPKPQKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRAtRKTSESRNLGKV
1	MSTNPKPQKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRaRKTSESRNLGKV
1	MSTNPKPQKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRNLGKV
1	MSTNPKPQKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRNLGKV
1	MSTNPKPQKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRtRKTSESRNLGKV
1	MSTNPKPQKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRNLGKV
1	MSTNPKPQKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSESRNLGKV
1	MSTNPKPQKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRAtRKTSESRNLGKV
1	MSTNPKPQKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRAtRKTSESRNLGKV
191-197	consensus

SEQ ID NO:	ISOLATE
194	Z5
193	Z1
192	Z8
195	Z6
196	Z7
191	Z4
197	DK13
191-197	consensus

FIGURE 7H-2

SEQ ID NO:	ISOLATE		
194	Z5	123	IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINYATGNLPGCSFSIFLLALFS
193	Z1	123	IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS
192	Z8	123	IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS
195	Z6	123	IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS
196	Z7	123	IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINYATGNLPGCSFSIFLLALLS
191	Z4	123	IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS
197	DK13	123	IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRILEDGvNYATGNLPGCSFSIFLLALLS
191-197	consensus		IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS

SEQ ID NO:	ISOLATE		
194	Z5	184	CLTTPASA
193	Z1	184	CLTTPASA
192	Z8	184	CLTVPASA
195	Z6	184	CLTVPtSA
196	Z7	184	CLTVPASA
191	Z4	184	CLTVPASA
197	DK13	184	CLTVPASA
191-197	consensus		CLTvPaSA

FIGURE 71-1

SEQ ID NO:	ISOLATE	
205	SA11	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
202	SA3	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
198	SA4	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
199	SA5	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
200	SA7	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
203	SA13	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
201	SA1	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
204	SA6	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
198-205	consensus	MSTNPKPQRKTKRNTNRRPQDVKFPGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
SEQ ID NO:	ISOLATE	
205	SA11	62 RQIPKARQPTGRSWGQPGYPWPfYANEGLGAGWLLSPRGSRPnWGPNDPRRrSRNLGKV
202	SA3	62 RQIPKARQPTGRSWGQPGYPWPfYANEGLGAGWLLSPRGSRPnWGPNDPRRrSRNLGKV
198	SA4	62 RQIPKARQPTGRSWGQPGYPWPfYANEGLGAGWLLSPRGSRPnWGPNDPRRrSRNLGKV
199	SA5	62 RQIPKARQPTGRSWGQPGYPWPfYANEGLGAGWLLSPRGSRPnWGPNDPRRrSRNLGKV
200	SA7	62 RQIPKARQPTGRSWGQPGYPWPfYANEGLGAGWLLSPRGSRPnWGPNDPRRrSRNLGKV
203	SA13	62 RQIPKARQPTGRSWGQPGYPWPfYANEGLGAGWLLSPRGSRPnWGPNDPRRrSRNLGKV
201	SA1	62 RQIPKARQPTGRSWGQPGYPWPfYANEGLGAGWLLSPRGSRPnWGPNDPRRrSRNLGKV
204	SA6	62 RQIPKARQPTGRSWGQPGYPWPfYANEGLGAGWLLSPRGSRPnWGPNDPRRrSRNLGKV
198-205	consensus	RQIPKARQPTGRSWGQPGYPWPfYANEGLGAGWLLSPRGSRPnWGPNDPRRrSRNLGKV

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FIGURE 71-2

SEQ ID NO:	ISOLATE	
205	SA11	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDDGVNYATGNLPGCSFSIFILALLS
202	SA3	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDDGVNYATGNLPGCSFSIFILALLS
198	SA4	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDDGVNYATGNLPGCSFSIFILALLS
199	SA5	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDDGVNYATGNLPGCSFSIFILALLS
200	SA7	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDDGVNYATGNLPGCSFSIFILALLS
203	SA13	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDDGVNYATGNLPGCSFSIFILALLS
201	SA1	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDDGVNYATGNLPGCSFSIFILALLS
204	SA6	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDDGVNYATGNLPGCSFSIFILALLS
198-205	consensus	IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDDGVNYATGNLPGCSFSIFILALLS
SEQ ID NO:	ISOLATE	
205	SA11	184 CLTVPATA
202	SA3	184 CLTVPASA
198	SA4	184 CLTVPASA
199	SA5	184 CLTVPASA
200	SA7	184 CLTVPASA
203	SA13	184 CLTVPTSA
201	SA1	184 CLIPASA
204	SA6	184 CLTVPASA
198-205	consensus	CLTVPASA

SEQ ID NO:	Genotype	cons.
155-206	97	LLSPRGSRpSwGptDPRrrSRnlgkVIdTlTCgfADLMGYiPlVGaPlGGvArALAHGVRvJEDGvNyATGNlPGcSfSIFlLlAlLScltvpAsa
155-176	type 1	LLSPRGSRpSwGptDPRrrSRnlgkVIdTlTCGFADLMGYiPlVGaPlGGaPaRALAHGVRvJEDGvNyATGNlPGcSfSIFlLlAlLScltvpAsa
177-186	type 2	LLSPRGSRpSwGptDPRHrSRnlgkVIdTlTCgfADLMGYiPvVGaPvGGvARALAHGVRvJEDGvNyATGNlPGcSfSIFlLlAlLScltvpAsa
181-190	type 3	LLSPRGSRpSwGpNDPRrrSRnlgkVIdTlTCGFADLMGYiPlVGaPvGGvARALAHGVRvJEDGvNyATGNlPGcSfSIFlLlAlLScltvpAsa
191-197	type 4	LLSPRGSRpSwGpNDPRrrSRnlgkVIdTlTCGFADLMGYiPlVGaPvGGvARALAHGVRvJEDGvNyATGNlPGcSfSIFlLlAlLScltvpAsa
198-205	type 5	LLSPRGSRpSwGpNDPRrkSRnlgkVIdTlTCGFADLMGYiPlVGpPvGGvARALAHGVRvJEDGvNyATGNlPGcSfSIFlLlAlLScltvpAsa
206	type 6	LLSPRGSRpSwGpNDPRrrSRnlgkVIdTlTCGFADLMGYiPlVGaPlGGvAALAHGVRvJEDGvNyATGNlPGcSfSIFlLlAlLScltvpAsa

FIGURE 7K-1

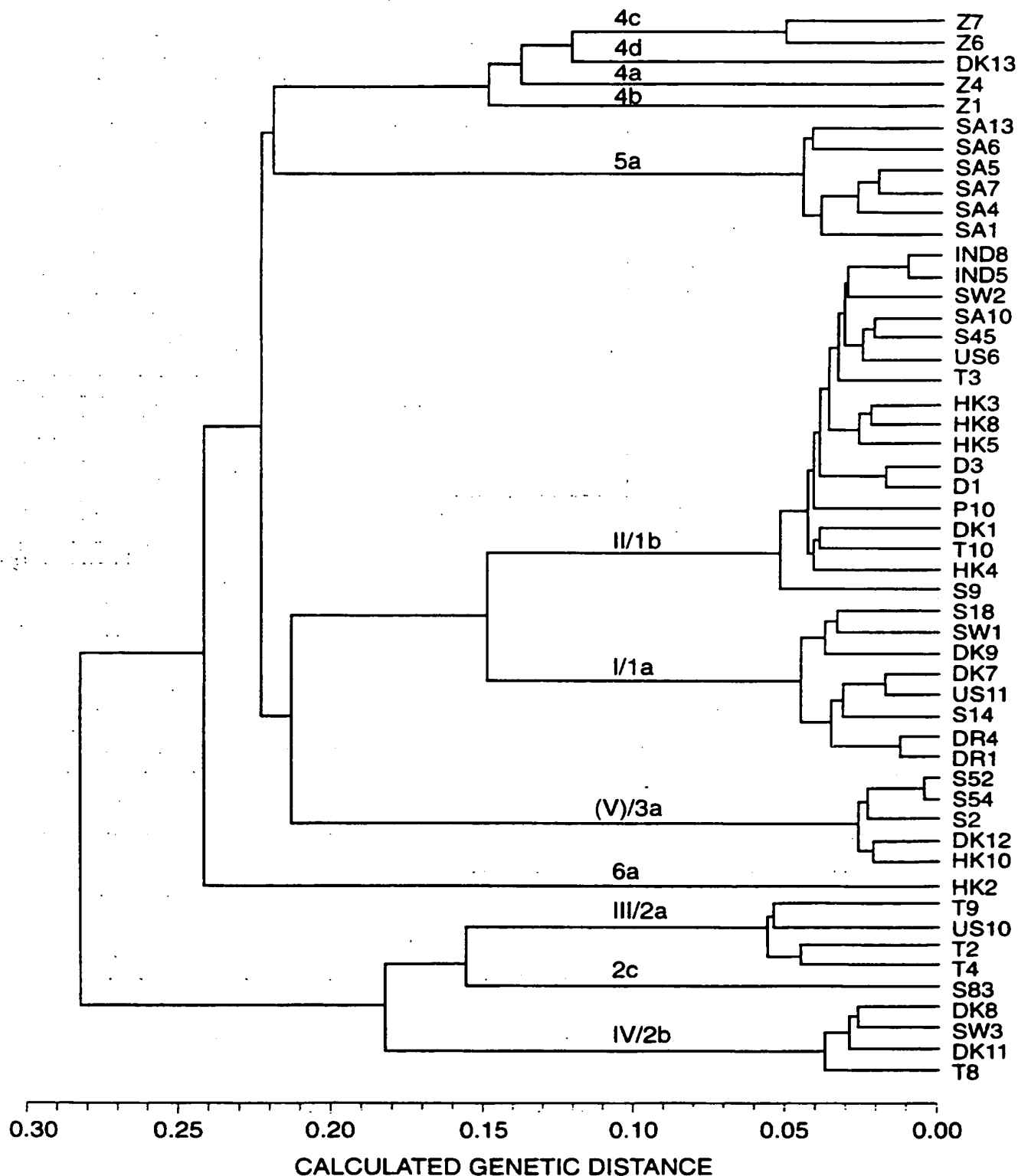
SEQ ID NO:	Genotype								
155-160	1/1a								
161-176	11/1b								
177-180	11/2a								
181-185	1V/2b								
186	2c								
187-190	(V)/3a								
191	4a								
193	4b								
194	4c								
195	4d								
197	4e								
198-205	5a								
192	4f								
199-205	5a								
206	6a								
MSTNPKPQRKTKRNTNRPPQVKKFPGGG/VGGVYLPRRGPRIGVBRATKTKTSERSOPRRROP1PKARPEGSVAQCPPLPYGRGCGWAGW									
10	11	20	30	40	50	60	70	80	90
--N--	K-K-	NR-Q-V-	L--	L--	AT-T-	L--	RPE-RT-AQ-Y-	L-GN-CG--	
--n--	K-K-	NR-Q-V-	L--	L--	AT-T-	L--	RPE-RQ-AQ-Y-	L-GN-mG--	
--n--	K-K-	NR-Q-V-	L--	L--	AT-T-	L--	RAT-KS-GK-Y-	L-GN-LG--	
--N--	K-K-	NR-Q-V-	L--	L--	AT-T-	L--	RST-KS-GK-Y-	L-GN-CG--	
--N--	K-K-	NR-Q-V-	L--	L--	AT-T-	L--	RTT-KS-GR-Y-	L-GN-LG--	
--L--	K-K-	TR-Q-V-	V--	L--	AT-T-	L--	RSE-RS-AQ-Y-	L-GN-CG--	
--N--	K-K-	NR-M-V-	L--	L--	AT-T-	L--	RPE-RS-AQ-Y-	L-GN-CG--	
--N--	K-K-	NR-M-V-	L--	L--	AA-T-	L--	RSE-RS-AQ-Y-	L-GN-CG--	
--N--	K-K-	NR-M-V-	L--	L--	AT-T-	L--	RSE-RS-AQ-Y-	L-GN-CG--	
--N--	K-K-	NR-M-V-	L--	L--	AT-T-	L--	GLE-RS-AQ-Y-	L-GN-CG--	
--N--	K-K-	NR-M-V-	L--	L--	AT-T-	L--	RSE-RS-AQ-Y-	L-GN-CG--	
--N--	K-K-	NR-M-V-	L--	L--	AT-T-	L--	RSE-RS-AQ-Y-	L-GN-CG--	
--L--	K-K-	NR-Q-V-	L--	L--	AT-T-	L--	Opt-RS-GQ-Y-	L-AM-LG--	
--L--	K-K-	NR-T-V-	L--	L--	AT-T-	L--	Opt-RQ-AQ-Y-	L-GN-CG--	

SSeq ID	NO:	Genotype
155-160	I/1a	LLSP-GS-PSuGpDPR-RR-L-K-L-GF-1-L-A-L-A-R-V-L-V-Y-L-S-L-L-LTV-ASA
161-176	I/1/b	LLSP-GS-PSuGpDPR-RR-L-K-L-GF-1-L-A-L-A-R-V-L-V-Y-L-S-L-L-LTV-asa
177-180	III/2a	LLSP-GS-PSuGpDPR-RR-L-K-L-GF-1-L-A-L-A-R-V-L-V-Y-L-S-L-L-LTV-ASA
181-185	IV/2b	LLSP-GS-PSuGpDPR-RR-L-K-L-GF-1-L-A-L-A-R-V-L-V-Y-L-S-L-L-LTV-ASA
186	2c	LLSP-GS-PSuGpDPR-RR-L-K-L-GF-1-L-A-L-A-R-V-L-V-Y-L-S-L-L-LTV-ASA
187-190	(V)/3a	LLSP-GS-PSuGpDPR-RR-L-K-L-GF-1-L-A-L-A-R-V-L-V-Y-L-S-L-L-LTV-ASA
191	4a	LLSP-GS-PSuGpDPR-RR-L-K-L-GF-1-L-A-L-A-R-V-L-V-Y-L-S-L-L-LTV-ASA
193	4b	LLSP-GS-PSuGpDPR-RR-L-K-L-GF-1-L-A-L-A-R-V-L-V-Y-L-S-L-L-LTV-ASA
195	4c	LLSP-GS-PSuGpDPR-RR-L-K-L-GF-1-L-A-L-A-R-V-L-V-Y-L-S-L-L-LTV-ASA
197	4d	LLSP-GS-PSuGpDPR-RR-L-K-L-GF-1-L-A-L-A-R-V-L-V-Y-L-S-L-L-LTV-ASA
198-205	4e	LLSP-GS-PSuGpDPR-RR-L-K-L-GF-1-L-A-L-A-R-V-L-V-Y-L-S-L-L-LTV-ASA
199	4f	LLSP-GS-PSuGpDPR-RR-L-K-L-GF-1-L-A-L-A-R-V-L-V-Y-L-S-L-L-LTV-ASA
202	5a	LLSP-GS-PSuGpDPR-RR-L-K-L-GF-1-L-A-L-A-R-V-L-V-Y-L-S-L-L-LTV-ASA
206	6a	LLSP-GS-PSuGpDPR-RR-L-K-L-GF-1-L-A-L-A-R-V-L-V-Y-L-S-L-L-LTV-ASA

FIGURE 8A



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FIGURE 8B

SUBSTITUTE SHEET (RULE 26)

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US 95/10398

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/51 C07K14/18 G01N33/53 A61K39/29 C12Q1/68
C12Q1/70 C07K16/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K G01N A61K C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	PROC. NATL. ACAD. SCI. USA., vol. 89, no. 11, June 1992 pages 4942-4946, JENS BUKH ET AL. 'Sequence analysis of the 5' noncoding region of hepatitis C virus.'	1,2,21, 31,32,38
Y	see the whole document	5-20, 22-30, 33-37, 39-51, 53,54, 56-59
	---	-/--

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- *A* document member of the same patent family

Date of the actual completion of the international search

20 February 1996

Date of mailing of the international search report

01.03.96

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Authorized officer

Hix, R

INTERNATIONAL SEARCH REPORT

Inter national Application No

PCT/US 95/10398

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	PROC NATL ACAD SCI U S A 90 (17). 1993. 8234-8238. CODEN: PNASA6 ISSN: 0027-8424, September 1993 BUKH J ET AL 'AT LEAST 12 GENOTYPES OF HEPATITIS C VIRUS PREDICTED BY SEQUENCE ANALYSIS OF THE PUTATIVE E1 GENE OF ISOLATES COLLECTED WORLDWIDE.'	1,2,5, 21-23, 26-32,38
Y	see the whole document	5-20,24, 25, 33-37, 39-51, 53,54, 56-59
X	--- JOURNAL OF GENERAL VIROLOGY 75 (5). 1994. 1053-1061. ISSN: 0022-1317, May 1994 SIMMONDS P ET AL 'Identification of genotypes of hepatitis C virus by sequence comparisons in the core, E1 and NS-5 regions.'	21,28
Y	see the whole document	1,2, 5-20, 22-27, 29-51, 53,54, 56-59
X	--- JOURNAL OF BIOMEDICAL SCIENCE 1 (3). 1994. 158-162. ISSN: 1021-7770, June 1994 KAO J-H ET AL 'Detection of divergent hepatitis C virus envelope sequences.'	21,28
Y	see the whole document	1,2, 5-20, 22-27, 29-51, 53,54, 56-59
X	--- BIOCHEM BIOPHYS RES COMMUN 192 (2). 1993. 635-641. CODEN: BBRCA9 ISSN: 0006-291X, 30 April 1993 STUYVER L ET AL 'ANALYSIS OF THE PUTATIVE E1 ENVELOPE AND NS4A EPITOPE REGIONS OF HCV TYPE 3.'	21,28
Y	see the whole document	1,2, 5-20, 22-27, 29-51, 53,54, 56-59

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 95/10398

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ARCHIVES OF VIROLOGY SUPPLEMENTUM 0 (7). 1993. 27-39. ISSN: 0939-1983, ROGGENDORF M ET AL 'Variability of the envelope regions of HCV in European isolates and its significance for diagnostic tools.'	21,28
Y	see the whole document	1,2, 5-20, 22-27, 29-51, 53,54, 56-59
X	--- PROC. NATL. ACAD. SCI. U. S. A. (1992), 89(15), 7144-8 CODEN: PNASA6;ISSN: 0027-8424, 1 August 1992 CHA, T. A. ET AL 'At least five related, but distinct, hepatitis C viral genotypes exist'	21,28
Y	see the whole document	1,2, 5-20, 22-27, 29-51, 53,54, 56-59
X	--- BIOCHEM. BIOPHYS. RES. COMMUN. (1994), 199(3), 1474-81 CODEN: BBRC A9;ISSN: 0006-291X, 30 March 1994 LI, JI-SU ET AL 'Identification of the third major genotype of hepatitis C virus in France'	21,28
Y	see the whole document	1,2, 5-20, 22-27, 29-51, 53,54, 56-59
X	--- WO,A,94 01778 (CHIRON CORP) 20 January 1994	53,54, 56-58
Y	see the whole document	1,2, 5-51,59
X	--- WO,A,92 19743 (CHIRON CORP) 12 November 1992	21,28
Y	see the whole document	1,2, 5-20, 22-27, 29-51, 53,54, 56-59
	--- -/--	

INTERNATIONAL SEARCH REPORT

 Internat'l Application No
 PC1/US 95/10398

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO,A,92 21759 (PASTEUR INSTITUT) 10 December 1992 see the whole document ---	1,2, 5-51,53, 54,56-59
X	EP,A,0 586 065 (TONEN CORP) 9 March 1994 see the whole document ---	53,54, 56-58
X	PROC. NATL. ACAD. SCI. USA, vol. 89, January 1992 pages 187-191, J. BUKH ET AL 'Importance of primer selection for the detection of hepatitis C virus RNA with the polymerase chain reaction assay' see the whole document ---	21,28
P,X	WO,A,95 01442 (US HEALTH) 12 January 1995 see the whole document ---	1,2, 5-51,53, 54,56-59
P,X	WO,A,94 25601 (INNOGENETICS NV ;MAERTENS GEERT (BE); STUYVER LIEVEN (BE)) 10 November 1994 see the whole document ---	21,28
Y	see the whole document ---	1,2, 5-20, 22-27, 29-51, 53,54, 56-59
P,X	WO,A,94 27153 (CHIRON CORP) 24 November 1994 see the whole document ---	21,28, 53-58
Y	see the whole document ---	1,2, 5-20, 22-27, 29-51,59
P,X	PROC. NATL. ACAD. SCI. U. S. A. (1994), 91(21), 10134-8 CODEN: PNASA6;ISSN: 0027-8424, 11 October 1994 STUYVER, LIEVEN ET AL 'Classification of hepatitis C viruses based on phylogenetic analysis of the envelope 1 and nonstructural 5B regions and identification of five additional subtypes' see the whole document ---	1,2, 5-51,53, 54,56-59

-/--

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 95/10398

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	JOURNAL OF CLINICAL MICROBIOLOGY 32 (9). 1994. 2280-2284. ISSN: 0095-1137, September 1994 RAVAGGI A ET AL 'Distribution of viral genotypes in Italy determined by hepatitis C virus typing by DNA immunoassay.' see the whole document ---	1,2, 5-51,53, 54,56-59
P,X	SEMINARS IN LIVER DISEASE, vol. 15, no. 1, February 1995 pages 41-63, J. BUKH ET AL. 'Genetic Heterogeneity of hepatitis C virus: Quasispecies and genotypes' see the whole document ---	1,2, 5-51,53, 54,56-59
P,X	BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 202, no. 3, 15 August 1994 pages 1308-1314, L. STUYVER 'Cloning and phylogenetic analysis of the core, E2 and NS3/NS4 regions of the hepatitis C virus type 5a+' see the whole document -----	1,2, 5-51,53, 54,56-59

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 95/ 10398

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 18,45,49
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although these claims are directed to a method of treatment of (diagnostic method practised on) the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

- 26 subjects

See continuation-sheets PCT/ISA/210

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1,2,5-51,53,54,56-59 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/SA/210

claims:

1. 1,2,5-51,53,54,56 to 59 (partially):

Genotypes specific peptides from E1 Seq. ID 1-8 and 52-59 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype I/1a.

2. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 103-108 and 155-160 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype I/1a.

3. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 9-25 and 60-76 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype II/1b.

4. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 109-124 and 161-176 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype II/1b.

5. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 26-29 and 77-80 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype III/2a.

6. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 125-128 and 177-180 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype III/2a.

7. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 30-33 and 81-84 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype IV/2b.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

8. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 129-133 and 181-185 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype IV/2b.

9. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 34 and 85 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype IV/2c.

10. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 134 and 186 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype IV/2c.

11. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 35-39 and 86-90 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype V/3a.

12. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 135-138 and 187-190 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype V/3a.

13. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 40 and 91 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4a.

14. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 139 and 191 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4a.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

15. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 41 and 92 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4b.

16. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 141 and 193 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4b.

17. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 42-43 and 93-94 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4c.

18. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 143-144 and 195-196 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4c.

19. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 44 and 95 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4d.

20. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 145 and 197 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4d.

21. 3-52,55 and 59 (partially):

Genotype specific peptides Core Seq. ID 142 and 194 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4e.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

22. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 140 and 192 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 4f.

23. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 45-50 and 96-101 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 5a.

24. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. 146-153 and 198-205 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 5a.

25. 1,2,5-51,53,54,56 to 59 (partially):

Genotype specific peptides from E1 Seq. ID 51 and 102 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 6a.

26. 3-52,55 and 59 (partially):

Genotype specific peptides from Core Seq. ID 154 and 206 used in the recombinant protein expression, detection of antibodies against HCV, vaccines and methods of detection using PCR primers and Identification of Genotype 6a.

INTERNATIONAL SEARCH REPORT

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